

142/615

FIGURE 141

AATGGCTGTCTTAGTACTCGCCTGACAGTTGCTGGACTGCTTGTCTTATTCTGACCTGCTATGCAGACGA  
CAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCAAGGCCAGACTTCCCCAAATTCTTAAG  
CCTCCTGGCACAGAGATCATTGAGAATGCAGTCGAGTTCATCCTCCGCTCCATGTCAGGAGCACAGGATTAT  
GGAATTGATGATAATGAAGGAAAACATTCAAAAGTGACATCCTCAGGACACACCCATGTTGGCTCCTGGACAA  
TCCAAGAGCAGCCAAATCTGCTTTCCAGTTGGCTCCACAAGTCCTCCAGGACAGAGGCCCTCAAAGCAACTCC  
CAACGAGTTCTCAGGATTCAAGGCTCTGGCTTCAACCAAACAGAACTCATTGAAACACCCCTGACTGCATTGGC  
TTTTAGAAAGTTAGAATAAATATGGCGTTGGGATCACATAGTTGATGGAGAGGAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

143/615

**FIGURE 142**

MAVLVRLTVVLGLLFLTCYADDKPDKPDDSGKDPKFSLLGTEIIENAVEFILRSMSRSTGFM  
EFDDNEGKHSSK

144/615

**FIGURE 143**

GGACGCCAGGCCCTGCAGAGGCTGAGCAGGGAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAGAGCTGGTCTG  
CCATGGACATCTGGTCCCCTGCAGCTGCTGGTCTGCTTACCCCTGCACCTCATGGCTCTGC  
TGGGCTGCTGGCAGCCCTGTGCAAAGCTACTTCCCCTACCTGATGCCGTGCTGACTCCCAAGAGCAACCGCA  
AGATGGAGAGCAAGAAACGGGAGCTTCAGCCAGATAAAGGGGCTTACAGGAGCCCTCCGGAAAGTGGCCCTAC  
TGGAGCTGGGCTCGGAAACGGGAGCCAACTTCACTTCACTCCACGGGCTGCAGGGTCACTGCCTAGACCCAA  
ATCCCCACTTGAGAACGTTCCCTGACAAGAGCATGGTGAAGAACAGGCACCTCCAAATATGAGCGGTTTGTGGTGG  
CTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTCTGCACTCTGGTCTGTGCTCTG  
TGCAGAGCCAAGGAAGGTCCCTGCAGGAGGTCGGAGAGTACTGAGACCGGGAGGTGTGCTCTTTCTGGGAGC  
ATGTGGCAGAACATATGGAAGCTGGGCTTCATGTGGCAGCAAGTTTCGAGCCCACCTGAAACACATTGGGG  
ATGGCTGCTGCCTCACAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCGAAATCCAATGGAACGAC  
AGCCCCCTCCCTGAAGTGGCTACCTGTTGGGCCCCACATCATGGAAAGGCTGTCAAACAATCTTCCCAAGCT  
CCAAGGCACACTATTTGCTCCTTCCCCAGCCTCCAATTAGAACACAAGCCACCCACCAGCCTATCTATCTTCCACTGA  
GAGGGACCTAGCAGAATGAGAGAACATTGATGACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC  
AATCTCTAACCTCAATCCCGCTTCGACAGTGAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGG  
ACCCCTGTTGATCCTCAACTGCAAGTTCTGGACTAGTCTCCCAACGTTGCCTCCCAATGTTGCTCCCTTCCTT  
CGTCCCCATGGTAAAGCTCTCGCTTCTCCCTGAGGCTACACCCATGCGTCTCTAGGAACGTGGTCAACAAAG  
TCATGGTGCTGCATCCCTGCCAACCCCCCTGACCCCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGCA  
CCAGGGAGAATCAGAGATGCTGGGATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTT  
TAATAAAATAGACGAAACCACG

145/615

FIGURE 144

MDILVPLLQLLVLLLTPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQIKGLTGASGKVALL  
ELGCGTGANFQFYPPGCRVTCLDPNPHFEKFITKSMAENRHLQYERFVVAPGEDMRQLADGSMDVVVCTLVLCSV  
QSPRKVLQEVRRLRPGGVLFFWEHVVAEPYGSWAFMWOQVFEPWKHIGDGCCLTRETWKDLENAQFSEIQMEROQ  
PPPLKWLPVGPHIMGKAVKQSFPSSKALICSFPSLQLEQATHQPIYLPLRGT

146/615

FIGURE 145

GTGGGATT TATTGAGTGCAAGATCGTTCTCAGTGGTGGAGTTGCCTCATCGCAGGCAGATGTTGGGC  
TTTGTCCGAACAGCTCCCTCTGCCAGCTCTGTAGATAAGGGTAAAGAACTAATATTATGACAGAAAGAAAA  
AGATGTCATTCCGTAAGTAAACATCATCATTGGCTGGCTGTTACTGGTTACAGATTAGGAATTGTAAGGGCCTCAACCTATAGACT  
ACTTCCTCAGCTTGAGCAGTTGTTAGGAATGAGGTTACAGATTAGGAATTGTAAGGGCCTCAACCTATAGACT  
TTGTCCCCAAATGCTCCGACATGGCAGTAGATGGAGAACAGAGGAGATTCTGTGGCTCATCCCTGCATCTGAAG  
ACAGGCTTGGGGGGCCATTGCAGCTATAACAGCATTCCGACAGAACACTCGCTCCAATGTGATTTCATCATTG  
TTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATAACAAAA  
TTGTCAATT TGACCCAAACTTTGAGGAAAGTAAAGGAGGATCTGACCAGGGGGAAATCCATGAAACCTT  
TAACCTTGCAAGGTTCTACTTGCCAATTCTGGTCCCAGCGCAAAGAAGGCCATATACTGGATGATGATGTA  
TTGTGCAAGGTGATATTCTGCCCTTACAATACAGCACTGAAGGCCAGGACATGCAGCTGCATTTCAGAAGATT  
GTGATTGCCTCTACTAAAGTTGTCACTCCGGAGCAGGAAACCGAGTACAATTACATTGGCTATCTGACTATA  
AAAAGGAAGAATTGTAAGCTTCCATGAAAGCCAGCACTGCTCATTTAACCTGGAGTTTGCAAAACC  
TGACGGAATGGAACGACAGAATAACTAACCAACTGAAAATGGATGAAACTCAATGTAAGAAGAGGGACTGT  
ATAGCAGAACCCCTGGCTGGTAGCATCACAAACACCTCCTGCTTATCGTATTTATCAACAGCACTCTACCATCG  
ATCCTATGTGGAATGTCGGCCACCTTGGTCCAGTGCTGAAAACGATATTCACCTCAGTTGTAAGGCTGCCA  
AGTTACTCCATTGGAAATGGACATTGAAGCCATGGGGAGGACTGCTCATATACTGATGTTGGGAAAAATGGT  
ATATTCCAGACCCAACAGGCAAATCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAACAGAA  
TTTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAGATAGCATGGAGTAACAGTTGCTAGGCTTC  
AATGCCTATCGGTAGCAAGCCATGGAAAAGATGTGTCAGCTAGGTAAAGATGACAAACTGCCCTGCTGGCAGT  
CAGCTCCCAGACAGACTATAGACTATAAAATGTCTCATGCCCTACCAAGTGTCTTACTACAATGCTG  
AATGACTGAAAGAAGAACTGATATGGCTAGTCAGCTAGCTGGTACAGATAATTCAAAACTGCTGTTTTA  
ATTTGTAAACCTGTGGCCTGATCTGTAATAAAACTACATTTTC

147/615

**FIGURE 146**

MSFRKVNIILVLAVALFLLVLHHNFLSILSSILRNEVTDSGIVGPQPIDFVPNALRHAVDGRQEEIPVVIASED  
RLGGAIAAINSIQHNTRSNVIFYIWTLNNTADHLRSWLNSDSLKSIRYKIVNFDPKLLEGKVKEPDQGESMKPL  
TFARFYLPILVPSAKKATYMDDVIVQGDILALYNTALKPGHAAAFSEDCDSASTKVVIRGAGNQNYIGYLDYK  
KERIRKLSMKASTCSFNPGVFVANLTEWKRNQITNQLEKWMKLNVEEGLYSRTLAGSITTPPLLIVFYQQHSTID  
PMWNVRHLGSSAGKRYSPQFVKAAKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLJRRYTEJSNIK

148/615

FIGURE 147

GTTTGAATTCCCTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCAGGCTACCAGTTCCCTCCAAGCA  
AGTCATTCCCTTATTAAACCGATGTGTCCTCAAACACCTGAGTGCTACTCCCTATTGCATCTGTTTGATAA  
ATGATGTTGACACCCCTCCACCGAATTCTAAGTGAATCATGCGGAAGAGATAACAATCCTGGCCTGTGATCC  
TCGCATTAGCCTTGTCTTGGCCATGATGTTACCTTCAGATTCACTACCCCTCTGGTACATTTTCAATTTCATT  
CATTGGTTATTGGGATTGTTGCTCGGGTGTATTATGGTGGCTGTATTATGACTATACCAACGACCTCA  
GCATAGAACATGGACACAGAAAGGAAAATATGAAGTGCGTGTGGGTTGCTATCGTATCCACAGGCATCACGG  
CAGTGCTGCTCGTCTGATTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTCAAATCACAAATA  
AAGCCATCAGCAGTGCTCCCTTCTGCTGTTCCAGCCACTGTGGACATTGCCATCTCATTCTCTGGTCC  
TCTGGGTGGCTGTGCTGAGCCTGGGAAC TG CAGGAGCTGCCAGTTATGGAAGGGCCAGTGGAAATATA  
AGCCCCTTCGGGCATTGGTACATGTGGTCGTACCATTAAATTGGCTCATCTGGACTAGTGAAATTCACTCTTG  
CGTGCCAGCAAATGACTATAGCTGGGCAGTGTTACTTGTATTCAACAGAAGTAAAATGATCCTCTGATC  
ATCCCATCCTTCGTCTCTCCATTCTCTCTACCATCAAGGAACCGTTGAAAGGGTCATTAAATCT  
CTGTGGTGAGGATTCCGAGAACATTGTACATGCAAAACGCCACTGAAAGAACAGCAGCATGGTGCAATTGT  
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTCTGGGTCTTGACAAAATACCTGCTCCATCTCAACCCAGAATG  
CATATACTACAACGTCTTAATGGACAGATTCTGTACATCAGCAGAAAGATGCAAAATCTTGTCAAGA  
ACTCAAGTCACTTTACATCTTAACGTTGGAGACTTCATAATTCTTAGGAAAGGTGTTAGTGGTGTGTT  
TCACTGTTTTGGAGGACTCATGGCTTTAACATCAGGCCATTCCAGGTGTGGCAGTCCTCTGTATTGG  
TAGCTTTTTGCCTACTTAGTAGCCCAGTTTATCTGTGTTGAAACTGTGCTGGATGCACTTTCTGT  
GTTTGCTGTTGATCTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTCTGAGTT  
TCGTAAAAGGAGCAACAAATTAAACATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGAGGGAA  
CAGAACTCCAGGCCATTGTGAGATAGATAACCCATTAGGTATCTGTACCTGGAAAACATTCTAAGAGCCA  
TTTACAGAATAGAAGATGAGACCAGAGAAAAGTTAGTGAATTTTAAAGACCTAATAAACCCATTTC  
TCCCTAAAA

149/615

**FIGURE 148**

MSGRDTILGLCILALALSLAMMFTFRFITTLLVHIFISLVLGLLFVCGVLWWLYDYTNDSLIEDTERENMKC  
VLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISAPFLLFQPLWTFAILIFFWVLWAVLLSLGTAG  
AAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWSEFILACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFY  
HQGTVVKGFLISVVRIPRIIVMMQNALKEQOHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTAINGTDFC  
TSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFVFGGLMAFNYNRAFQVWAVPLLVAFFAYLVVAHSFL  
SVFETVLDALFLCAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELOQAIVR

150/615

**FIGURE 149**

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTGGACCTCTCCCTGTTCTCTTGAATAATTGTAT  
TGGGATTGTGATGCAGGAAAGCTAACGGGAAAGGAAAGAATATTCAATTCTGTGTTGTTGAAAATTGAAAAAA  
ATTGCCCTCTTCAAACAAGGGTGTCAATTCTGATATTATGAGGACTGTGTTCTCACTATGAAGGCATCTGTTAT  
TGAAATGTTCTTGTGTTGCTGGTACTGGAGTACATTCAAACAAAGAACGGCAAGAAGATAAAAGGCCAA  
GTTCACTGTGCTCAGATCACTGGCATGTCAGGAAAGACATCTGATCCTGAGTTCATGAAATTGTGAAATGTCC  
AGCAGGATGCCAAGACCCAAATACCATGTTATGGCACTGTGATGCACTCTACTCCAGTGTGTTGGCG  
TGCCGTACACAGTGGTGTGCTGATAATTCAAGGAGGGAAATACTTGTGCGAAGGTTGCTGGACAGTCTGTTA  
CAAAGGGAGTTATTCCAACGGTGTCAATCGTTATCCCTACACAGTGGAGAGAAATCCTTATCGTCTTAGAAAG  
TAAACCCAAAAGGGTGTAAACCTACGGCTCTTACATCATCATCGAAAGTCCAGTGGCAAGCAG  
TGAGACACACAAAAGCTATCAGAGGCCACCTATTCCAGGGACAATGCACAGCGGTCACTGTGATGCAGCTCT  
GGCTGTCACTGTAGCTGGCACCCCCACCCACCTTGCAAGGCCATCCCTCTGCTGCTTCAACCACAGCAT  
CCCCAGACACAAATCAGTGGGCCACAGGCCAGGAGATGGATCTGGTCACTGCCCACCTACACAAGCGCCA  
AAACAGGCCAGGCTGATCCAGGTATCCAAAGGCAAGATCCTCAGGGACTGCGCTTCCAGAAACCTGTTGGAGC  
GGATGTCAGCTGGACTGTTCCAAAAGAAGAAATTGAGCACACAGTCTTGGAGGCCAGTATCCTGGAGATCC  
AAACTGCAAAATTGACTTGTGTTTAATTGATGGGAGCACAGCATGGCAAAAGGGCATTCCGAATCCAGAA  
GCAGCTCCIGGCTGATGTTGGCCAAGCTTGTGACATTGGGCTGCGGCTTCAACTGATGGGTTGTCAGTATGG  
AGACAACCCCTGCTACTCACTTAACTCAAGACACACAGAAATTCTGAGATCTGAAGAGACGCCATAGAGAAAAT  
TACTCAGAGAGGAGGACTTCTAACTGTAGGTGGGCCATCTCCTTGTGACCAAGAACTTCTTCCAAAGCCAA  
TGGAAACAGAAAGGGCTCCAACTGTGGTGTGATGGTGTGCTGGGCCACGGGACAAGTGGAGGAGGC  
TTCAAGACTTGGAGAGGACTGAGGAATCAACATTCTCATCACCATTGAGAGTGTGCTGAAATGAGAAGCA  
GTATGTGGTGGAGGCCAACTTGTGAAACAAGGGCTGTGCAAGAACAAACGGCTTCACTCGCTTCAACGTGCAAGAG  
CTGGTTTGGCTCCACAAGACCCCTGCAAGCTCTGGTGAAGCGGGTCTGGACACTGACCGCCTGGCTGCAAGCAA  
GACCTGCTTGAACACTGGCTGACATTGGCTTGCATCGACGGCTCCAGCAGTGTGGGACGGGCAACTTCCGCAC  
CGTCTCCAGTTGTGACCAACCTCACCAGGAGATTGAGATTTCGACACGGCACCGCAGTCAGCTGGGGCGTGC  
GTACACCTACGAACAGCGGCTGGAGTTGGTGTGACAAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAA  
GAGGGTGGGCTACTGGAGTGGTGGCACAGCACGGGGGCTGCCATCAACTTGGCTTCAAGCAGTCCGGATCCAGC  
GTGCAAGGCCAAACAGGAAGTTAATGATCCTCATCACCCAGCAGGGAGGTCTACGACGACGGCTTCAAGGAA  
CATGGCTGCCATCTGAAGGGAGTGTGACATTGGCTTGCATAGGCGTTGGCTGGCAAGAGGAGCTAGAAGT  
CATTGCCACTCACCCGCCAGAGACCACTCCTCTTGTGGAGAGTGTGACAAACCTCCATCAGTATGTCCCCAG  
GATCATCCAGAACATTGTGACAGGTTCAACTCACAGCCTGGAACTGAAATTGAGGAGCAGGAGCACAGCAA  
GTGCTGCTTACTAAGTGTGTTGGACCAACCCACCGCTTAATGGGGCACGGTGCATCAAGTCTGGGC  
AGGGCATGGAGAAACAAATGTTGTTATTATCTTGCATCATGCTTTTCAATTCCAAACTTGGAGTTAC  
AAAGATGATCACAAACGTATAGAATGAGCCAAAAGGCTACATGTTGAGGGTGTGGAGATTACATTGTGA  
CAATTGTTTCAAATAAATGTCAGGAATACAGTGCAGGCCATTACGACAGGCTTACGTAGAGCTTGTGAGATT  
TTAAGTGTGTTATTCTGATTTGAACTCTGTAACCTCAGCAAGTTCTGATGACAATGAGGAATTG  
CTGAATTAAATGTTAGAAGGATGAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG  
AAG

151/615

FIGURE 150

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAGCQDPKYHVG  
TDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWRESFIVLESKPKKGVTPSAL  
TYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVATPTTLPRPSAASTTSIIPRPQSVGRHSQE  
MDLWSTATYTSSQNRPRAADPGIQQRQDPSGAAAFQKPVGADVSIGLVPKEELSTQSLEPVSLGDPNCKIDLSSLIDG  
STSIGKRRFRIQKQILLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRA  
ISFVTKNFFSKANGNRSGAPNNVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAV  
CRTNGFYSLHVQSWFGLHHTLQPLVKRVCDTDRACSKTCINSADIGFVIDGSSSVGTGNFRTVLQFVTNLKEF  
EISDTDTRIGAVQTYEQRLEFGFDKYSSKPDILNAIKRVGWSSGGTSTGAAINFALEQLFKKSKPNKRKLMLI  
TDGRSYDDVRIPTAMAHLKGVITYAIGVAWAQQEELEVIATHPARDHSFVDEFDNLHQYVPRIIQNICTEFNSQPRN

152/615

**FIGURE 151**

CAGGATGAACGGTTGCAGTGGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTATGCCTTCCGGCT  
GCTCATCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGTGCGCCAGGTCCGACGGCTCCCGGCC  
AGATCCGCCACTACAGTTTCTCTGACTCTAATTGATGCACTGGACACCTTGCTGATTTGGGAATGTCTC  
AGAATTCAAAGAGTGGTGAAGTGCCTCAGGACAGCGTGGACTTGAATATTGATGTGAACGCCTCTGTGTTGA  
AACAAACATTGAGTGGTAGGAGGACTCTGTCTGCTCATCTGCTCTCAAGAAGGCTGGGTGGAAGTAGAGGC  
TGGATGGCCCTGTCGGGCCCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACCTCTCCCAGCCTTCAAGAC  
CCCCACTGGCATGCCATATGAAACAGTGAACCTACTCATGGCTGAACCCAGGAGAGACCCCTGTACCTGTAC  
GGCAGGGATTGGGACCTCATTTGTAATTGCAACCCCTGAGCAGCCTCACTGGTGACCCGTGTTGAAGATGT  
GGCCAGAGTGGCTTGATGCCCTCTGGAGAGGCCGGTCAGATATGGGCTGGTCCGAACCACATTGATGTGCT  
CACTGGCAAGTGGTGGCCAGGACGCAGGCATGGGGCTGGCTGGACTCCTACTTGAGTACTGGTGAAGAG  
AGCCATCCTGCTTCAGGATAAGAAGCTCATGGCATGTTCTAGAGTATAACAAAGCCATCCGAACATACACCCG  
CTTCGATGACTGGTACCTGTGGGTCAGATGTACAAGGGACTGTGTCCATGCCAGTCTTCAGTCCTGGAGGC  
CTACTGGCCCTGGTCTTCAGAGCCTCATGGAGACATTGACAATGCCATGAGGACCTCTCAACTACTACACTGT  
ATGGAAGCAGTTGGGGGGCTCCCGGAATTCTACAACATTCTCAGGGATAACACAGTGGAGAAGCGAGAGGGCTA  
CCCACTTCGCCAGAACCTATTGAAAGCGCAATGTACCTTACCGTGCACGGGGATCCCACCCCTCTAGAAACT  
CGGAAGAGATGCTGTGGAAATCCATTGAAAAAAATCAGCAAGGTGGAGTGCAGGATTGCAACAATCAAAGATCTGCG  
AGACCCACAAGCTGGACAACCGCATGGAGTCGTTCTGGCCAGACTGTGAAATACCTTACCTCTGTTGA  
CCCAACCAACTCATCCACAACAATGGGTCACCTCGACCGGTGATCACCCCTATGGGAGTGCACTCTGG  
GGCTGGGGGGTACATCTCAACACAGAACGCTCACCCCATCGACCTGCGCCCTGCACTGCTGCCAGGGCTGAA  
GGAAGAGCAGTGGGAGGGTGGAGGACTTGATGGGAATTCTACTCTCAAACGGAGCAGGTGAAATTTCAGAA  
AAACACTGTTAGTTGGGGCCATGGAACCTCCAGCAAGGCCAGGAACACTCTTCTCACCAGAAAACCATGACCA  
GGCAAGGGAGAGGAAGCCTGCCAACAGAAGGTCCCACCTCTCAGCTGCCAGTCAGCCCTCACCTCCAAGTT  
GGCATTACTGGGACAGGTTTCTAGACTCCTCATAACCACTGGATAATTTTTATTGGAGGCT  
AAACTATAATAATTGCTTTGGCTATCATAAAAA

153/615

FIGURE 152

MPFRLLIPIGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVEVLQDSVDFIDVN  
ASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPILLRMAEEAARKLLPAFQTPTGMPYGTVNLLHGVPNPG  
PVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALMRLWESRSRSDIGLVGNHIDVITGKWAQDAGIGAGVDSYFE  
YLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDWYLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFL  
NYYTWWKQFGGLPEFYNIPOQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECGFAT  
IKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYIFNTEAHPIDLAALHC  
CQRLKEEOWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPSQP  
FTSKLALLGQVFLDSS

154 / 615

**FIGURE 153**

CGGACGCCTGGCGGACCGTGGCGGACGCCTGGGTTGGGAGGGGCAGGATGGGAGGGAAAGTGAAGAAAACA  
GAAAAGGAGAGGGACAGAGGCCAGAGGACTTCATACTGGACAGAAACCGATCAGGC**ATGGA**ACTCCCCTCGT  
CACTCACCTGTTCTGCCCCCTGGTGTCTGACAGGTCTGCTCCCCCTTAACCTGGATGAACATCACCCACG  
CCTATTCCCAGGGCCACCAGAAGCTGAATTTCGATACAGTGCTTACAAACATGTGGGGTGACAGCGATGGAT  
GCTGGTGGCGCCCTGGGATGGCGCTCAGGCAGGGGAGGGGACGTTATCGCTGCCCTGTAGGGGGGC  
CCACAATGCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGAAATTCACTCATCCTGCTGTGAATAT  
GCACCTGGGATGTCTGTTAGAGACAGATGGTGTGGGGATTATGGTGAAGCT**AAGGAGAGGGTGGCAG**  
TGTCTCTGAAGGTCCATAAAAGAAAAAGAGAACTGTGGTAAGGGAAATGGTCTGTGGAGGGGTCAAGGAGT  
TAAAAAACCTAGAAAGAAAAGGTAGGTATGTCAGGGAGTAGTCTCATGCCCTTCACACTGGGAGCATGTT  
TGAGGGTGCCTCCCAAGCCTGGGAGTAATTTCCCCCATCCCCAGGCCTGTGCCCTCTGGTCTCGTGC  
TGTGGCAGCTCTGTCTCAGTTCTGGGATATGTGCCGTGTGGATGCTTCATTCCAGCCTCAGGGAAAGCCTGGCA  
CCCACTGCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTCCCAGAAGGAGATACTGGTGGGAAAAGATG  
GGGCAAAGCGGTATGATGCCCTGGCAAAGGGCCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCT  
CCATGTTCTAACAGATTCAAGACTCCTGGCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGC  
CAAGGTGGGCAGATCACTTGAGGTCAAGGACCAAGCCTGGCAACATGGTGAACACTCCATCTACTAA  
AAAAAAAAAAATACAAAAATTAGCTGGGTGCGCTAGTGCAATGCCCTGTAATCTCATCTACTGGGAGGCTAAGACA  
GGAGACTCTCACTCAACCAGGGTGGAGCTTGCGGTGAGCCAAGATTGTGCCCTGCACTTAGCGTGGGTG  
ACAGAGTAAGCGAGACTCCATCTAAAAATAATAATAATTCAACTCCTTATCAGGAGTCCATGATCTG  
GCCCTGGCACAGTAACTCATGCCCTGTAATCCCAACATTGGGAGGCAACGCAGGAGGATTGCTTGAGGTCTGGA  
GGTTTGAGACCAGCCTGGCAACATAGAAAGACCCATCTCTAAATAATGTTTAAAAAT

155/615

**FIGURE 154**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039  
><subunit 1 of 1, 124 aa, 1 stop  
><MW: 13352, pI: 5.99, NX(S/T): 1  
MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPWDGPGSGDRRGDVYR  
CPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMLGMSLLETDGDGGFMVS

**Important features:**

**Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 70-73

**N-glycosylation site.**

amino acids 98-101

**Integrins alpha chain proteins**

amino acids 67-81

156/615

**FIGURE 155**

GGCAGCTCCGGGTGCTGGCCCCGGCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGAGGCTCCAGCTGC  
ACGTCCTCCCGCCCGCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCCCTCGGGACCAAACAAGCCTGGCAGG  
GTCTCACTTGTGCCCAGGCTGGAGTTCACTGCCCCATGATCATGGTTACTGCAGGCTTGACCTOCTGGGTTCAA  
GCGATCCTGCTGAGTAGCTGGGACTACAGGACAAAATGAAGATCAAATGGAAAATATGCTGCTTGGGTTGAT  
ATTTCACCCCTGGGTGGACCCCTATTGATGGATCTGAAATGGAATGGGATTATGTGGCAGTTGAGAAAGGT  
ACCCCGGATTGTCACTGAAAGGACTTCCATCTCACCAAGCCCCGATTGAGGCAGATGCTAAGATGATGGTAAA  
TACAGTGTGTGGCATGCAATGCCAGAAAGAACCTCCAACTCCAGCCTTCTGAATGGAGGATTATCTTCCATA  
TGAGACTGTCTTGAGAATGGCACCCGAACCTTAACCAGGGTAAAGTCAAGATTTGGTTCTGAGCCGACTCA  
AAATATCACCACAAAGGGAGTATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTCAAGCATCTT  
GGACAAAAGTTCTAACCAATTCCCTTTAGCACAGCTGTGAAGCTTCCACGGGCTGTAGTGGCATTCTCAT  
TTCCCTCAGCATGTTCAACTGCTGCCACTGTGTTCATGATGGAAAGGACTATGTCAAAGGGAGTAAAAGCT  
AAGGGTAGGGTTGTTGAAGATGAGGAATAAAGTGGAGGCAAGAACGTCAGGGTCTAAGAGGAGCAGGAGAGA  
AGCTAGTGGTGGTACCAAGAGAGGGTACCAAGAGAGCATCTGCAGGAGAGCGAAGGGTGGGAGAAGAAGAAA  
AAAATCTGGGGGGGTAGAGGATTGCCAGGGAGGCCTCCTTCAGTGGACCCGGGTCAGAAGAATACCCACAT  
TCCGAAGGGCTGGGAGGGCATGGGGAGCTACCTGGACTATGACTATGCTTCTGGAGCTGAAGCG  
TGCTCACAAAAGAAATCATGGAATCTGGAATCAGGCAACGATCAAGAAAATGCTGGTGGAAATGATCCACTT  
CTCAGGATTGATAACGATAGGGCTGATCAGTTGGTCTATGGTTTGCAGTGTGCCAGCAATCCAATGATCT  
CCTTACCAAACTGCGATGCTGAGTCGGGCTCCACGGTCTGGGGICTATCTGCGTCTGAAAGATCCAGACAA  
AAAGAATTGGAAGCGAAAATCATGCGGTCTACTCAGGGCACCAGTGGTGGATGTCACGGGTTCTAGAAGGA  
CTACAACGTTGCTGTTGCATCACTCCCTAAATACGCCAGATTGCTCTGGATTCACGGGAACGATGCCAA  
TTGTGTTACGGCTAACAGAGACCTGAAACAGGGCGGTATCATCTAAATCACAGAGAAAACAGCTCTGCTTA  
CCGTAGTGAGATCACTCATAGGTTATGCCCTGGACTTGAACCTGTCAATAGCATTCAACATTTCAAATCA  
GGAGATTTCGTCCATTAAAAATGTATAGGTGAGATATTGAAACTAGGTGGGACTTCATGCCAAGTATAT  
ACTCTCTTACATGGTGTGAGTTCAATTGTTAGAAAAATTGTTGCTCTTAAATTAGACACACTTTAA  
ACCTTCAAACAGGTATTATAAAATACATGTGACTCCTTAATGGACTTATTCTCAGGGTCTACTCTAAGAAGAAT  
CTAATAGGATGCTGGTTGTGTTAAATTGTAAGATAAGGATGCTGAAAGCAATTAGTACCTGAAAGAAT  
ATAGAGACAGAAAAGTTACAACACAGTTGTACTCTGAGATGGATCCATTGAGCTCATGCCCTCAATGTTAT  
ATTGTGTTATCTGTTGGGTCTGGGACATTAGTTAGTTTGAAGAATTACAATCACAGAAGAAAAGCAAGC  
ATTATAACAAAACATAAAACTGTTTACTGCTTAAGAAATAACAATTACAATGTGTTATTATTTAAAATGGGA  
GAAATAGTTGTTCTATGAAATAACCTAGTTAGAAATAGGGAAGCTGAGACATTAAAGATCTCAAGTTTTA  
TTAACTAATACTCAAATATGGACTTTCATGTATGCATAGGAAGACACTTCACAAATTATGAATGATCATGT  
GTGAAAGCCACATTATTTATGCTATACATTCTATGTGAGGTGCTACATTTTAGGACAAGAATTCTGAA  
TCTTTTCAAGAAAGAGCTTTCTCCTGACAAATCCAGCTTTGTATGAGGACTATAGGGTGAATTCTCTG  
ATTAGTAATTAGATATGCTTCTCTAAATGAATAAAATTATGAATATGA

157/615

**FIGURE 156**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253
<subunit 1 of 1, 413 aa, 1 stop
<MW: 47070, pI: 9.92, NX(S/T): 3
MENMLLWLIFFTPGWTLIDGSEMWEWDFMWHLRKVPRIVSERTFHLTSPAFEADAKMMVNTVC
GIECQKELPTPSL
SELEDYLSYETVFENGTRTLTRVKQDLVLEPTQNITTKGVSVRKRVQVYGTDSRFSILDKRFLTN
FPFSTAVKL
STGCGILISPOHVLTAAHCVHDGKDVKGSKKLRVGLLKMRNKSGGKRRGSKRSRREASGGDQREGT
REHLQE
RAKGGRRKKSQRGQRIAEGRPSFWTRVKNTHIPKGWARGGMGDATLDYDYLALLELKRAHKKYME
LGISPTIK
KMPGGMIHFSGFDNDRADQLVYRFCVSDESNDLLYQYCDAESGSTGSGVYRLKDPLKNWRKIIA
VYSGHQW
VDVHGQKDYNVAVRITPLKYAQICLWIHGNDANCAYG
```

**Important features:**

**Signal peptide:**  
amino acids 1-16

**N-glycosylation sites.**  
amino acids 90-93, 110-113 and 193-196

**Glycosaminoglycan attachment site.**  
amino acids 236-239

**Serine proteases, trypsin family, histidine active site.**  
amino acids 165-170

158/615

FIGURE 157

GGGACCCATCGGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGCAGCGGACAAAGGAGCATGTCGCG  
CGGGGGAAAGGCCGTCTCCGGCCGCCATAAGCTCCGGTGCAGCGCTGGGCCGCGCCGCGCTCTGCCCGCCCG  
GGCTCCGGGGCGGCCCGCTAGGCCAGTGCAGCGCTGCCCGCAGGCCCGCAGCAGCATGGAGCACC  
GGACGCCGGCGGGGCCGCGCAGGCCGCTGGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGA  
GGCGCGGGCGGCCGCGCAGGCCGCTGCCCGCAGCAGCATGGGCCGAGGGCGAGGGCTGCGAG  
GCCGGCGGGCGGCCGAGGGCAAGGTGGTGTGCAAGCAGCTGGACTGCCGAGGTCTGCCCGAGAATACTCTG  
CCAACCGCACGGTACCCCTGATTCTGAGTAACAATAAGATGCCAGCTGAAGAATGGCTATTCTGGGTTA  
AGTCTCTTGAAAGATTGGACCTCGAACAACTTATTAGTAGTATAGATCCAGGTGCTTCTGGGACTGTCA  
TCTCTAAAAGATTGGATCTGACAAACAATCGAATAGGATGTCTGAATGCAGACATATTGAGGACTACCAAT  
CTGGTCTGGCTAAACCTTCGGGAAATTGTTCTTCATTATCTCAAGGAACCTTGTGATTATCTTGCCTGCTTCA  
CGGTCTTGGAAATTCCAGACTGAGTATCTTGTGTGACTGTAACATACTGTGGATGCATCGCTGGTAAAGGAG  
AAGAACATCACGGTACGGGATACCAGGTGTTTATCTAAGTCACTGCAGGCCAACAGTCACAGGCCTGAAG  
CAGGAGCTGTTGACATGCGACCCCTCGCTTGAAATTGCGCTTCTACATGACTCATCTCATGCCAAGTTGTG  
TTTGAAGGAGACAGCCTCCCTTCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGATCAG  
GATGGGAGAATAGTGAACACGATGAATCGCAAGGTATTGTTGTGAAAGAACATGATTCAACTGCTCCCTG  
ATTGCAAGTGGCTAACCATCTTAATTCAAGGCTGGATCTACTGGAAATTGGGCTGTCATGTCCAGACCAAA  
CGTGGGAAATAACAGGAGCTGTGATATTGGTGTGATATTAGAGAGTCTGCACAGTACTGTCTCCAGAGAGGGTG  
GTAAACAAACAAAGGTGACTTCAGATGGCCCAGAACATTGCAGGCAATTACTGCATATCTGCAGTGTACGGAAAC  
ACCCATGGCACTGGCATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTGGGCCAGATGTGATAGAGGTGGC  
TTTGGGCAAGTGTGATTATTCTCGCTGTGACTGCAAATGATGTCACTAGAGTTCTTATATGTTAACAG  
ATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTGACAGTTACTGGCTTACACTGTGGAAGCAGCCAACCTT  
TCTGACAAAATGGATGTTATATTGTCAGAAATGATTGAAAAATTGGAAGATTACCAAGGAGAAAATCA  
AAAGAGCTAGGTGACGTGATGGTGCACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCCTGTGGCTGGCG  
CAGAGGGAAAGCTAAAGCCCTGCAGTAGGATTGTCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTGG  
GCTCACGTTATTCAACATATTCAACCCATATTGCTCTGGAGCTTATGTCATCAAGTCTACTGGCTTCACGGGG  
ATGACCTGTACCGTGTCCAGAAAGTGGCAGCTGAGCTTAAAGTCAATGTTCAAGTCTGGCAGTAAAGGTA  
TGTTACATTCTGCAATCAATTAAAGACTATTACAGT**TAA**ATTAGAATGCTCAAATGTTCTGCTTCGCAAATAA  
CCTTATTAAAAGATTTTTTGCAAGGAAGATAGGTATTGCTACTGTTAAAGAAAACAAACCA  
GAAGAACTGCATTACGACTTCAAGGGCCCTAGGCATTGGCCTTGATTCCCTTCTCACATAAAATATCA  
GAAATTACATTATAACTGCACTGGTATAATGCAAATATACTATTGTTACATGTGAAAAAATTGACT  
TAAAAGTTATTATTGTTCTGCTCTGATTTAAGACAATAAGATGTTCTGATGGGCCCTAAAGTATC  
ATGAGCCTTGGCACTGCGCTGCAGCCTAGTGGAGAAGTCAACCCCTGAGACCAGGTGTTAATCAAGCAAG  
TGTATATCAAATTTGGCAGAAAACACAAATATGTCATATATCTTTTAAAGGATATTCAAGCA  
AGCAAAATGAAAGCATTTACTGATTAAAATTGGTGTGTTAGATATAATTGACTACACTGATTGAAGCAA  
ATAGAGGAGGACAACACTCCAGCACCCTAATGAAACCACATTTCACCTAGCTTCTGCTGGCATGTGTAATT  
GTATTCTCTGCGGTTTAATCTCACAGTACTTTATTCTGCTTGTCCCTCAATAATCACAACAAATATTCC  
AGTCATTAAATGGCTGCAATAACTGATCCAACAGGTGTTAGGTGTTAGTGTGAGCACTCAATAAA  
TATTGAATGAATGAACGAAAAAAAAAAAAAA

159/615

**FIGURE 158**

MEPPGRRRGRAQPPLLPLSLLALLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGKVVCSSLELAQVLP  
PDTLPNRTVTLLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGAFWGLSSLKRLLDLTNNRIGCLNADIFR  
GLTNLVRLNLSGGNLFSSLSQGTFDYLASLRSIEFQTEYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLSQAOPV  
TGVKQELLTCDDPPELPSFYMTPSHRQVVFEQDSLPFQCMASYIDQDMQVLWYQDGRIVETDESGIFVEKNMIH  
NCSLIASALTISNIQAGSTGNWGCHVQTKRGNNRTVDIVVLESSAQYCP PERVNNKGDFRWPRTLAGITAYLQ  
CTRNTHGSGIYPGNPDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPINLTNAVATARQLAYTVE  
AANFSDKMDVIFVAEMIEKFGRTKEEKSKELGDVMDIASNIMLADERVLWLAQREAKACSRIVQCLQRiatYR  
LAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCTVFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSL  
ALKVCYILQSFKTIYS

**Signal peptide:**  
amino acids 1-33

**Transmembrane domain:**  
amino acids 13-40 (type II)

**N-glycosylation site.**  
amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336, 433-437,  
453-457, 592-596

**N-myristoylation site.**  
amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57, 57-63, 99-105,  
123-129, 142-148, 162-168, 317-323, 320-326, 384-390, 403-409, 554-560

160/615

**FIGURE 159**

GGGGAAATCTGCAGTAGGTCTGCCGGC**GATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGGCTGCTGTTGTC**  
**CTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTCAAAATGGAAAGTATTATTGACCAAATTAAACAGG**  
TCTTTGGAGAATTACGAACCATGTCAAGTCAAAACTGCAGCTGCTACCATGGTGTCAAGAAGAGGATCTA  
CCTTCCGAGGGAGGCATCTCCAGGAAGATGATGGCAGAGGTAGTCAGACGGAAAGCTAGGGACCCACTATCAGATC  
ACTAAGAACAGACTGTACCGGGAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTATTTG  
GAAGT GATCGGGCGTCTCCCTGACATGGAGATGGTGTCAATGTACGAGATTATCCTCAGGTTCTAAATGGATG  
GAGCCTGCCATCCCAGTCTTCCTCAGTAAGACATCAGAGTACCATGATATCATGTATCCTGCTGGACATT  
TGGGAAGGGGACCTGCTGTTGCCAATTATCCTACAGGTCTGGACGGTGGGACCTCTCAGAGAACATCTG  
GTAAGGT CAGCAGCAGTGAAAAGAAAAACTCTACAGCATATTCCGAGGATCAAGGACAAGTCCA  
GAACGAGATCCTCTCATTCTCTGCTCGGAAAAACCCAAAACCTGTTGATGCAGAAATACACCAAAAACAGGCC  
TGGAAATCTATGAAAGATACTTAGGAAAGCCAGCTGCTAAGGATGTCATCTTGATGACTGCAAATACAAG  
TATCTGTTAATTTCGAGGCAGTGTGCAAGTTCCGGTTAAACACCTCTCCTGTGTGGCTCACTTGT  
CATGTTGGT GATGAGTGGCTAGAAATTCTCTATCCACAGCTGAAGCCATGGGTTCACTATACCCAGTC  
GATCTCTCCAATGTCCAAGAGCTGTTACAATTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGG  
GGAAGGCCAGTTATTAGGAACCATTGCAAGATGGATGACATCACCTGTTACTGGGAGAACCTTGTGAGTGAATAC  
TCTAAATTCTGCTTATAATGTAACGAGAACGGTTATGATCAAATTATCCCCAAATGTTGAAAACGTGAA  
CTATAGTAGTCATCATAGGACCATAGTCCTTTGTGGCAACAGATCTCAGATATCCTACGGTGAGAACGTTACC  
ATAAGCTTGGCTCCATACCTGAAATATCTGCTATCAAGCCAAATACCTGGTTTCTTATCATGCTGCACCCAG  
AGCAACTCTGAGAAAGATTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTGATGAATAAGG  
ACCAGAAATCGTGAGATGTGGATTGAAACCCACTCTACCTTCTATTCTTAAGACCAATCACAGCTGTGCC  
TCAGATCATCCACCTGTGTGAGTCATCACTGTGAAATTGACTGTGCCATGTGATGATGCCCTTGTCCATT  
TTGGAGCAGAAAATTGTCATTGGAAAGTAGTACAACCTATTGCTGAAATTGTGAAATTATCAAGGCGTGATC  
TCTGTCACTTATTAAATGTTAGGAAACCTATGGGTTATGAAAATACTTGGGATCATCTGTAATGGTC  
TAAGGAAGCGGTAGCCATGCAATGATGTTAGGAGTTCTCTTTGTAACCAACTCTGTTACTCAGGA  
GGTTCTATAATGCCACATAGAAAGAGGCCAATTGCAATTGATGAGTAATTATTGCAATTGGATTCTAGGTTCCCTTT  
GTGCCATTGCTCATGCCCTACTTCTTAATGCCCTCTAAAGCCAA

161/615

FIGURE 160

MEWWASSPLRLWLLLFLLP SAQGRQKESGSWKVFI DQINRSLEN YEPCSSQNCS CYHGVIEEDLTPFRGGISRK  
MMAEVVRRKLGTHYQITKNR LREND CMFPSRCGVEHFILEVIGRLPD MEMVINVRDYPQVPKWM EPAIPVFSF  
SKTSEYHDIMYPAWTFWEGGP AVWP IYPTGLGRWDLFREDLIVRSAAQWPWKKKNSTAYFRG SRTSPERDFLILLS  
RKNPKLVDAEYTKNQAWKSMKDTL GKPAAKDVHLVDHCKYKYL FNFRGVAASFRFKHLFLCGSLVFHVGD EWLEF  
FYPQLKPWVHYIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFISYNVT  
RRKGYDQIIIPKMLKTEL

162/615

FIGURE 161

CCGAGGCACAGGAGATTGCCCTGGCTGGCTGGAAAAGCTATCAAGGAAGAAATTGCCAAA  
CCATGTCTTTTTCTGTTTAGAGTAGTTACAACAGATCTGAGTGTAACTAAGCATGGAATACAGAAAA  
CAACAAAAACTTAAGCTTAATTCACTGGAAATTCCACAGTTCTTAGCTCCCTGGACCCGGTTGACCTGTT  
GGCTCTTCCCGCTGGCTGCTCATCACGTGGTGCTCCGACTACTCACCCGAGTGTAAAGAACCTTCGGCTCG  
CGTCTGAGCTGCTGTGGATGGCTCGGCTCTGGACTGTGCTTCAGTAGGATGTCAGTGGATCCCTC  
AAATGGAGCCTCTGCTGTCACCTCGAGTTCTTGTGATGTGGTACCTCAGCCTTCCCCACTACAATGTG  
ATAGAACGCGTGAACGGATGTAACCTCTATGAGTATGAGCCATTACAGACAAGACTTCACACTTCGA  
GAGCATTCAAACGTCTCATCAAATCCATTCTGGTCACTCCACCCCTCAGATGTGAAAGCC  
AGGCAGGCCATTAGAGTTACTTGGGGTAAAAAGTCTGGTGGGATATGAGGTTCTTACATTTTCTTATTA  
GCCAAGAGGCTGAAAAGGAACACAAAATGTGGCATTGCTTAGAGGATGAACACCTTCTTATGGTACATA  
ATCCGACAAGATTTTACACATATAAACTGACCTTGAACCCATTATGGCATTCAAGCTGGGTAACTGAG  
TTTGCCCCATGCCAAGTACGTAACTGAGACAGACACTGATGTTCTCATCAACTTGCAATTAGTGAAGTAT  
CTTTAAACCTAAACCCTAGAGAAAGTCTGGTCACTTCTCTAATTGATAATTATCCTATAGAGGATT  
TACCAAAACCCATATTCTTACAGGAGTACCTTCAGGTGTTCCCTCATACTGCAGTGGGTTGGGTTAT  
ATAATGTCCAGAGATTGGTCCAAGGATCTATGAAATGATGGGTCACTGAAACCCATCAAGTTGAAGATGTT  
TATGTGGGATCTGTTGAATTATTAAAGTGAACATTCAATTCCAGAAGACACAAATCTTCTTATAT  
AGAATCCATTGGATGTCGCAACTGAGACGGTGTGATTGCAAGCCATGGCTTCTTCCAAGGAGATCATCACT  
TTTGGCAGGTCATGCTAAGGAACACCATGCCATTATTAAACTTCACATTCTACAAAAGCCTAGAAGGACAGG  
ATACCTTGTGGAAAGTGTAAATAAAAGTAGGACTGTGGAAAATTCTATGGGGAGGTCAGTGTGCTGGCTTACACT  
GAACTGAAACTCATGAAAACCCAGACTGGAGACTGGAGGGTACACTTGTGATTATTAGTCAGGCCCTCAA  
GATGATATGTGGAGGAATTAAATATAAGGAATTGGAGGGTTTGCTAAAGAAATTAGGACCAAACAATTG  
GACATGTCAATTCTGTAGACTAGAATTCTTAAAGGGTGTACTGAGTTATAAGCTACTAGGCTGTAAAAACAA  
ACAATGTAGAGTTTATTGAAACATGTACTGAAAGGTTTGCTATATCTTATGTGGATTACCAATT  
TTAAAATATATGTAGTTCTGTGTCAAAAAAACTCTTCACTGAAGTTACTGAACAAAATTTCACCTGTTTG  
GTCATTATAAGTACTTCAAGATGTTGCACTGAAGTTACTGAACTTAAAGTAAACTTCAACTTGTGTT  
TTAAATGTTGACGATTCAATACAAGATAAAAGGATAGTGAATCAATTCTTACATGCAACATTTCCAGT  
TACTTAACTGATCAGTTATTGATAACATCACTCCATTAAATGTAAGTCAGGTCATTATGCAATATCAGTA  
ATCTCTGGACTTGTAAATATTACTGTGGAATATAGAGAATTAAAGCAAGAAAATCTGAAAA

163/615

**FIGURE 162**

MASALWTVLPSRMSLRSILKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQDFHFTLREHSNC SH  
QNPFLVILVTSHPSDVKARQAIRVTWGEKKSSWGYPEVLTFFLLGQEAEKEDKMLALSLEDEHLLYGDIIIRQDFLD  
TYNNLTLKTIMAFRWVTEFCPNAKYVMKTDTDFINTGNLVKYLLNLNHSEKFFTGYPLIDNSYRGFYQKTHIS  
YQEYPFKVFPPYCSCGLGYIMSRDLPRIYEMMGHVVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVC  
QLRRVIAAHGFSSKEIITFWQVMLRNTTCHY

164/615

FIGURE 163

CATTTCTGAAACTAATCGTGTAGAATTGACTTTGAAAAGCATTGCTTTTACAGAAGTATATTAACCTTTAGG  
AGTAATTCTAGTTGGATTGTAATATGAAATAATTAAAGGGCTCGCTCATATATAGAAAATCGCATATGG  
TCCTAGTATTAAATTCTATTGCTTACTGATTTTGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTG  
AATATAAAATAAGAGAAGAAAAAGAATAAAAGTAGATTGAGTCTCCAATTATGTAAGCTCAGAAGAACTGGTT  
TGTGTTACATGCAAGCTTATAGTTGAAATATTTCAGGAATTACATGAATGACAGTCTCGAACCAATGTGTTG  
TTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACCTCAGATTCCGTTGCCAA  
CTCGTCCCCATTGGTTCTTCTTGGTACTACAGAAGAGGAATCCAGGAATCTGCATAGAAACACTTAGGC  
TTTATACAGAAAAAGCAAACATGAATTACTGGAAAAGAAGTAGAAAAAGAAGTAGCCTACAAGAAG  
CCAAATTAAAGCAAAGGGATTGAATCCGGATGGAACCTCCAGCCCTTCAACCCTGGGTGGATTTCAGCCT  
CCAAGCCATCATCACCAGAGAAGTAAAGCTGAAGAGAAATCACCACATCTCCATTAAATGTGAAGACAGTCAAA  
AAGAACCTGAGGATAGACAACAGGCTTCAAAGAACGATCACGTTCTAGATCACACTTCCAAGAACAGACT  
ATAAGCAGAAGTCGAAGTCGATCGAGGTCAAGAACACGATCACGTTCTAGATCACACTTCCAAGAACAGACT  
ATAATAGGGCGAGTCGATCTGGACATACAGCTCGAGATCAAGAACGGTCCCGCAGTCACAGTGAAAGCCCTC  
GAAGACATCATATCATGGTCTCCTCACCTAAGGCCAACGATCACAGAGATGATTAAAAGTCAAAACAGAC  
ATGGTCATAAAAGGAAAAAAATCTCGTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAGCCAAGAAC  
ACAGGCATGAAAGGGGACATCATAGGCACAGGCGTGAACGATCTCGTCTTGGAGAGGTCCCATAAAAGCAAGC  
ACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCGCTGACTTCTCTTGGAGCTGCATCAGTTCT  
TGGTTTGCCTATCTACAGTGTGATGACTCAATCAAAACATTAAACGCAAACGATTAGGATTTGATT  
CTTGAAACCCCTCTAGGTCTCTAGAACACTGAGGACAGTTCTTTGAAAAGAACTATGTTAATTTCAGC  
TAAAATGCCCTAGCAGTATCTAATTAAAACATGGTCAGGTTCAATTGACTTTATTATAGTTGTTAATTGTT  
AATGCTATAAGAACCTGGAGCGTGAATTCTGTTAAAATGATGGTGAATACCTTCTTAACACTGGTTGCTGC  
TCTATTAAAGTGGTTATTGTTAAATGATGGTGAATACCTTCTTAACACTGGTTGCTGCATGTGTAAGATT  
TTTACAAGGAAATAAAATACAAATCTGTTTCTAAAAAAAAAAAGT

165/615

**FIGURE 164**

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLFGTTEEEIQEICIETLRLYTRKKPNYELLEKE  
VEKRKVALQEAKLKAKGLNPDGTPALSTLGGFPASKPSSPREVKAEKSPISINVKTVKKEPEDRQQASKSPYN  
GVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYNNRSGTYSSRSRSRSRSHSESPRRHNGSPHLKAKH  
TRDDLKSSNRHGHKRKKSRSRSQSKSRDHSDAAKKHRHERGHHRDRERSRSFERSHKSKHHGGSRGHGRHRR

166 / 615

**FIGURE 165**

GGTTCCTACATCCTCATCTGAGAATCAGAGAGCATATACTCTACGGGCCGTGATTATTAACGTGGCTTA  
ATCTGAAGGTTCTCAGTCAAATTCTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTGCTAAAGGAGCTT  
GGCTGGTTGGGCCCTTGTAGCTGACAGAAGGTTGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGC  
TTCTGTGCTGGTCTTGCCCTGGCTCAGTCAGTACATTGACAATGTGGCAACCTGCACTTCTGTATT  
CAGAACTCTGAAAGGTGCCTCCACTACGCCGTGACCAAAGATAGGAAGAGGGCCTCACAGATGGCTGCCAG  
ACGGCTGCGAGCCTCACAGCACGGCTCCCTCCCCAGAGGTTCTGCAGCTGCCACCCTCCTTAATGACAG  
ACGAGCCTGGCTAGACAACCCCTGCCTACGTGTCCTGGCAGAGGACGGCAGGCCAGCAATCAGCCCAGTGGACT  
CTGGCCGGAGAACCGAACCTAGGGCACGGGCCCTTGTAGAGATCCACTATTAGAACGAGATCATTAAAAAAATAA  
ATCGAGCTTGTGTTCTCGAAAGGACAAGAGCGGGAGTGCAGTTGCCAACATGCCAGGCCAGGGCAGGGAAA  
ATTCTGAAACACCAACTGCCCTGAACTTCTCAAGGTTGATCCACCTGATTCCAGATGGTAAATTACCAAGCA  
TCAAGATCAATCGAGTAGATCCAGTGAAGGCCTCTCTATTAGGCTGGTGGAGGTAGGAAACCCACTGGTCC  
ATATCATTATCCAACACATTATCGTGTGGGTGATGCCAGAGACGGCCGCTACTGCCAGGAGACATCATT  
TAAAGGTCAACGGGATGGACATCAGCAATGTCCTCACAACACTACGCTGTGCGTCTCTGCCAGGCCCTGCCAGG  
TGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGCAGCAGGAACAATGGACAGGCCGGATGCCATACAGAC  
CCCGAGATGACAGCTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAAATAAAACTGGTGC  
AGGTGGATGAGCCTGGGGTTTCACTTCAATGTGTCGGATGGCGGTGTCATGACATGGTCACTTGAGG  
AGAATGACCGTGTGTTAGGCCATCAATGGACATGATCTTCGATATGCCAGGCCAGAAAGTGGCTCATGATT  
AGGCCAGTGAAGAGCCTGTCACCTCGTGTCCCCCAGGTTGGCAGGGAGCCCTGACATCTTCAGGAAG  
CCCGCTGGAAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGAGAGGAGCAACACTCCAAAGCCCCCTCATC  
CAATTACTTGTGATGAGAAGGTTGAAATATCCTAAAGACCCGGTGAATCTCTCGGATGACCGTGCAGGG  
GAGCATCACATAGAGAATGGGATTGGCTATCTATGTCATCAGTGTGAGGCCGGAGGAGTCAAAAGCAGAGAT  
GAAGAATAAAACAGGTGACATTGGTGAATGTGGATGGGTCGAACTGACAGAGGTGAGCCGGAGTGGAGG  
TGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTGGAAAGTCAGGAACTGATGAG  
ACTGCAGCAGCCCAGCAGCCCTGGACTCCAACCAACATGGCCCCACCCAGTGAATGGTCCCCATCTGGGTCA  
TGTGGCTGGAAATTACCAACGGTGTGTTGATAACTGTAAAGATATTGATTACGAAGAAACACAGCTGGAAAGTCTGG  
GCTTCTGCATTGTAGGGAGGTTATGAAGAATACAATGGAAACAAACCTTTTCAATCCATTGTTGAAGGAA  
CACCAGOATACAATGATGGAAGAATTAGATGTGGTGAATTCTTCTGCTGTCATGGTAGAAGTACATCAGGAA  
TGATACATGCTGCTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTCTGGC  
GCACCTTTTA**TAGA**ATCAATGATGGTCAAGGAAACAGAAAATCAGAAATAGGCTAAAGAAGTGAACACT  
ATATTTATCTTGTGATGTTTATATTAAAGGAAGAATTACTCTAACTATTGTTCTGGC  
TGAAAGCAGTACACCTCAGAAAATGATTCCAAAATGAGTCAAGGAAAGTGTGAGGAG  
TTCTCATACTCTACAAACATTGTTATTTCTATTCAATAAAAGGCCCTAAAACACTAAAATGATTGATT  
TGTATACCCACTGATTAAGCTGATTTAAATTGGTATATGCTGAACTGCTGCCAGGGTACATT  
GGCCATTAAATTACAGCTAAATATTGTTAAATGCAATTGCTGAGAACAGTGTGTTCAAAACAAGAAT  
AAATTTTCAAGGTTAA

167/615

**FIGURE 166**

MKALLLVLWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCAISLTATAPSPEVSAATIS  
LMTDEPGLDNPAYVSSAEDGQPAISPVDGRSNRTRARPFERSTIRSRSFKKINRALSVLRTKSGSAVANHADQ  
GRENSENTTAPEVFPRLYHLIPDGIEITSIKINRVDPSESLSTRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPG  
DIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVMREQFRSRNNGQAPDAYRPRDDSFHVIINKSSPEEQLGIK  
LVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRSPDI  
FQEAGWNSNGSWSPGPERSNTPKPLHPTITCHEKVNIIQKDGPESLGMTVAGGASHREWDLPIYVISVEPGGV  
SRDGRIKTGDILLNVDGVELTEVSERSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPPSDWSP  
SWVMWLELPRLYNCKDIVLRRNTAGSLGFCIVGGYEYNGNKPFIFIKSIVEGTPAYNDGRIRCVDILLAVNGRS  
TSGMIHACIARLLKELKGRTLTIVSWPGTFI

168/615

**FIGURE 167**

GGGAAAGCCATTCGAAAACCCATCTATACAAACTATATTTCATTCTGCTGCTAGCTGCCTTGGCCTCAC  
AATTTCAATTCTGTTCTGACTTCAGTTATACCGTGGATGGAGTTGATCCAAACCATAACATCGTGGAG  
GGTTTAATTTGGTAGCCCTCACCAATTCTGGTGTGGCTTCTTGAGAGGATTCCACCTCAAAATCA  
TGAACCTGGCTGTTGATCAAAGAGAATTGGATTCTACTCTAAAGTCATAAGGACTGGCAAAAGAAGCT  
ACCAGAAGACTCAACCTGGCCTCCATAAACAGGACAGATTATTCAAGGTGATGGCAAAATGGATTCTACATCAA  
CGGAGGCTATGAAAGCCATGAACAGATTCCAAGAAACTCAAATTGGGAGGCCAACCCACAGAACAGCATT  
CTGGGCCAGGCTGTAATCAGAATTGTCGTCGATGCTCAACAGCATTGCTTTTCCCCAAATTAAACACATT  
GTGGAGAAGTGTGATGATACTCTCCCTTACCTTCCCTCTCCATTCAAGCATTCAAAGTATATTTCATGAATT  
AAACCTTGAGCAAGGGACCTTAGATAGGCTTATTCTGACTGTATGCTTACCAATGAGAGAAAAAAATGCATT  
CCTGTATCATCCTTTCAATAAAACTGTATTGAAAAAAAAAAAAAA

169/615

FIGURE 168

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHEIWLLIKREFGFYSKSQYRTWQKKLAEDSTWPPINRTDY  
SGDGKNGFYINGYESHEQIPKRKLKLGGQPTEQHFWARL

170/615

**FIGURE 169**

171/615

**FIGURE 170**

MELGCWTQLGLTFLQLLLSSLPREYTVINACPGAEWNIMCRECCSEYDQIECVCPGKREVVGYTIPCCRNEENE  
CDSCLIHPGCTIFENCKSCRNGSWGTLDDFYVKGFYCAECRAGWGGDCMRCGQVLRAPKGQILLESYPLNAHC  
EWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQIIRKRCGNERPAPIQSIGSSLHVLFHSDGSKN  
FDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI  
NGRHAKIGTVVSFFCNNSYVLSGNEKRTCQONGEWSGKQPICIKACREPDKISDLVRRRVLPMQVQSRETLHQLY  
SAAFSKQKLQSAPTKKPALPFGLPMGYQHLHTQLQYECISPFYRLGSSRRTCLRTGKWSGRAPSCIPICGKIE  
NITAPKTQGLRWPWQAIIYRRTSGVHDGSLHKGAWFLVCSCALVNERTVVVAACVTDLGKVTMIKTADLKVVLG  
KFYRDDDRDEKTIQSLQISAIILHPNYDPILLADIAILKLLDKARISTRVQPICLAASRDLSTSfqeshitvag  
WNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVDNMFCASWEPTAPSdictaetggiaavsfpg  
RASPEPRWHLMGLVWSWSYDKTCSHRLSTAFTKVLPKDWIERNMK

172/615

FIGURE 171

CTGTCGTCTTGCTTCAGCCGCACTGGCTGCCACTGGCTGCCAGGTGCTTACAGCCTGTTCCAAGTGTGGCTTA  
ATCCGTCTCCACCACCAAGATCTTCTCCGTGGATTCCCTCTGCTAAGACCGCTGCCATGCCAGTGA  
CACCGCCATCACAAACCAACGACGTCATCTCGGGCTGGGGTCCCCATGATCGTGGGGTCCCCTCGGGCCCT  
GACACAGCCCCCTGGGTCTCCCTCGGCTCGAGCTGGTCTACCTCGCTGCCCTCTCGCTGGTGGCTAGCGT  
GGCGCCTGGACGGGTCCATGGCAACTGGTCCATGTTCACCTGGTCTCTGCTTCTCGGTGACCGT  
CCTCATCGTGGAGCTGTGCGGGCTCCAGGCCGCTCCCCCTGCTGGCGCAACTTCCCATCACCTCGCCTG  
CTATCGGGCCCTCTCTGCCTCTCGGCTCCATCATCACCCACCACTATGICCAGTTCCTGTCCCACGGCCG  
TCGCGGGACCACGCCATGCCGCCACCTCTCTCGCATCGCGTGTGGCTTACGCCACCGAACGGCTG  
GACCCGGGCCCCGGCCCGAGATCACTGGTATATGGCACCGTACCCGGCTGCTGAAGGTGCTGGAGACCTT  
CGTTGCCTGCATCATCTCGCTTCATCAGCAGCCCAACCTGTACCGACCCAGCCGCTGGAGTGGTGC  
GGCGGTGACGCCATCTGCTTCATCCTAGCGGCCATGCCATCTGCTGAACCTGGGGAGTGCACCAACGTGCT  
ACCCATCCCTCCCCAGCTCTGTGCGGGCTGGCTTGCTGTCTGCCTCTATGCCACCGCCCTGTTCT  
CTGGCCCCCTCTACCAAGTTCGATGAGAAGTATGGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGAG  
CCATGCCACTACGTGCTGCTGGGACCCGGCAGCTGGCTGTGGCCATCCCTGACGCCATCAACCTACTGGCGTA  
TGTGGCTGACCTGGTGCACTCTGCCACCTGGTTTGTCAAGGTCTAAGACTCTCCCAAGAGGCTCCCTGTTCC  
TCTCCAACCTCTTGTCTTCTGCCCCAGTTCTTATGGAGTACTTCTTCTCCGCTTCCCTGTTCT  
CTCTCCCTGCTCCCTCCCTCCACCTTTCTTCTCCCAATCCTGACTCTAACAGTTCTGGATGC  
ATCTTCTTCTCCCTTCTGCTGTTCTCTGTGTTGTTGTTGCCCCACATCCTGTTTACCCCTG  
AGCTGTTCTCTTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT  
CTCTCCCTGCTCCCTCCCTCCACCTTTCTTCTCCCAATCCTGACTCTAACAGTTCTGGATGC  
TCTTTCTGGGTGCTGCTGGCTTCTTATCTGCCGTGTTGCAAGCACCTCTCTGTGCTGCC  
GAGACTCTTCTCTCTGCCCTCCACCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTG  
ATGCCACAGCCCCCAAGGGGCCATTGCCAAAGCATGCCCTGCCACCCCTCGCTGTGCTTAGTCAGTGT  
GTGTGTGTGTGTGTGTGTTGGGGGGTGGGGTAGCTGGGATTGGGGCTCTTCTCCAGTGGAGGAA  
GGTGTGCAGTGTACTTCCCCCTTAAATTAAAAACATATATATATATATATTTGGAGGTCA  
GCGGGAGGCATTAAGCACCGACCCCTGGGTCCCTAGGCCCGCCTGGCACTCAGCCTGCC  
AATTTTGCAGGCTTACAGAACACCACTGCCAGAGGCCATCTTAAAGGAAGCAGGGCTGGATGC  
CCCAACTATTCTGTGGTATGAAAAG

173/615

**FIGURE 172**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTTRTTTTTSSSGLGSPIVGSPRALTQPLGLRLQLVSTCVAFSLVASVGAWTGSMGNWSMFTWCFC
FSVTLLIIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIYPTTYVQFLSHGRSRDHAIATFFSCIACVA
YATEVAWTRARPGEITGYMATVPGLLKVLETFVACIIFAFISDPNLYQHQPALEWCVAVVYACIFILAAIAILLNL
GECTNVLPPIPFPFSFLSGLALLSVLLYATALVLWPLYQFDEKYGGQPRRSRDVCSRSHAYYCAWDRRLLAVALT
AINLLAYVADLVHSAHLVFKV
```

**Important features:****Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-  
255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21

174/615

**FIGURE 173**

GAACGTGCCACCAGCCCAGCTAATTTGTATTTTAGTAGAGACGGGTTTACCATGTTGCCAGGGCTGGTC  
 TTGAACCTCGTACCTCATGATCCGTCACCTCGGCCTCCAAAGTGTGGATTACAGGCATGAGCCACTGACGC  
 CTGGCCAGCCTATGCATTTAAAGAAATTATTCTGTATTAGGTGCTGTGCTAACACATTGGCACTACAGTGACCA  
 AAACAGACTGAATTCCCCAAGGCCAAAGACCAGTGAGGGAGACCAACAAGAAACAGGAAATGCAAAGAGACCA  
 TTATTACTCACTATGACTAAGGGTACAAATGGGTACGTTGATGGAGAGTGATTGTTAAAGAGACTACAGAGGG  
 AGGACAGACTACCAAGAGGGGGCCAGGAAAGCTCCTCTGACGAGGTGGTATTGAGCCAAACTGGAAGAATGA  
 GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGAGCACTACACTCACTACACTTTGGCCTGAGAA  
 AATAGCATGGGATTGGAGGAGGCTGGGGAAACACCACTCTGCCACCTGGGCAGGAGGATTGAGGGCTTGAGA  
 AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGGACAGGGACTTGCAAGGTGGAATCATTAGGTCTTATC  
 AACAGATATGGGCAAGCAAAGCCAGGGAGAATTGATGTTAATGTCAGGTTGGAGCCAGGCTAGATGGGACAG  
 TGGGGGTGATGCAAAGGAAAGAGGTGAGGAAGCAGGGCAGACGTCAGGGAGAAGGGTGTGGGGGTTGGGTTCCA  
 TCTTGGCAGCTGCGGAATGTTGATGGGAAGACCAAGAGGAGGAGGAGCAAGGGCAGAGGGGAAGGGAATCTAA  
 AGAACTCTGGATGCAACACTCTCTTCTCTTCT  
 TTCTGCCCCCTGCCTCCATCTCTCTGGGTGCTGGAAAGTGGAGGATTAGCTGAAGTTTGCTTCTCGGGGCTG  
 TCTGAATCTCCATTGCTTCTGGGAGGACATAATTCACTGTCTAGCTCTCTCTCATGCCCTTGCTGGGTATGGGATGTTAG  
 CCACTGGGACATATGTTGTTCTCTAGCTCTGTCTCTCTCATGCCCTTGCTGGGTATGGGATGTTAG  
 GGGGAAGGTCAATTGCTGTCAAGAGGGCACTGACTTTCTAATGGTGTACCAAGGTGAATGTTGGAGACACAGTC  
 GCGATGCTGCCAAGTCCCAGCGAGCCCTAACATATCCAGGAGATGCGTGCCTGCCAGGTCCCTGCATGGT  
 ATGCAAGCCCTCCCAATGTTCTGCCACTTGTCTTCTCTCCCGTTGCACTCCCTTGGGACTTGGAACTGTTCT  
 GTGAGTACATGCTGGGTCTCCCTTCTCTCTGCTCAGGTGAATCTCAGGCCCTCTCCACCCAAAGGTTC  
 ACATGGGATCTTAACACTGCAACCTTCCACCTCCCTGCTCAGGTGCTCCCTGCTCCCTGCTTACCGGCTTC  
 TCCACCCCTCCCTATCTCCAGGTATTCTCCAGGTGGTGAAGGAGCACCGTGAACCGCTACCGCCATGGCCAGG  
 GCGAGTGGCTCACCTCATTGAGTGGAAAGGGCTGGAGCAAGCCGAGTGAACCTGCTGCCCTGGAATCAGCCT  
 TTTCTCTTCTATTCAAGACCTCAGCGAGGGCAACAAGAGGCTCGCTTGTCAAGCAGGAGTGGCTGAGCAGTTGCCA  
 TCGCGGAAGCCAAGCTCCGAGCATGGTCTCGGTGGATGGCGAGGACTCCACTGATGACTCTATGATGAGGACT  
 TTGCTGGGGAATGGACACAGACATGGCTGGCAGCTGCCCTGGGCCGACCTCCAGGACCTGTCACCGGCC  
 ACCGGTTCTCCGGCTGTGCCAGGGCTCCGTGGAGGCTGAGAGCGACTGCTCACAGACCGTGTCCCCAGACA  
 CCCTGTGCTCTAGTCTGTGCACTGGAGGATGGGTGTTGGGCTCCCGCCGGCTGCCCTCCAGCTGCTGG  
 GCGATGAGCTGCTCTGCCAAACTGCCCTCCAGGCCGGAAAGTGCCTCCGCAAGCCTGGGCACTGGAGGCC  
 AGGACTCACTACAACACTGCCCTCACAGAGTCTGCCTTCCCGCCGGAGGAGGAGGCCAGGCCCTGCAAGG  
 ACTGCCAGCCACTCTGCCCTAACGGCAGCTGGGAACGGCAGGCCAACGCTCTGACCTGCCCTTCTCTG  
 GGGTGGTGTCTTAGTGGAGGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 GCGATGAGCTGCTCTGCCAAACTGCCCTCCAGGCCGGCTGCTGGGGCTCAAGGCTCCAGCAGAGCTCCACAGC  
 TAGAGGGCTCTGGGAGCGCTCGCTCTCCGGTGTGTGTTTGCAATGAAAGTGTGTTGGAGAGGAGGAGGAGG  
 GGCTGGGGCGCATGCTCTGCCCTACTCCCGGCTTGCCGGGGGTGCCCCGGGCTCTGGGAGGAGGAGGAGG  
 GCTGTGGCAGACAGTGATGTTCATGTTCTAAATGCCACACACATTTCTCTCGGATAATGTAACCAACTA  
 AGGGGTTGTGACTGGGCTGTGTGAGGGTGGGTGGAGGGGGCCAGCAACCCCCCACCCTCCCCATGCCCTC  
 TCTTCTCTGCTTTCTCACTCCGAGTCATGTGCACTGCTGATAGAAATCACCCCCACCTGGAGGGCTGG  
 CTCTGCCCTCCCGCCTATGGGTGAGCCGTCCTCAAGGGCCCTGCCAGCTGGCTGCTGTGCTTC  
 ATTCACTCTCCATGCTCTAAATCTCTCTTTCTAAAGACAGAAGGTTTTGGCTGTTCTCAGTC  
 GGATCTCTCTCTGGGAGGCTTGGATGATGAAAGCATGTCACCTCCACCCCTTCTGGCCCCCTAATGG  
 GCCCTGGGGCCCTTCCCAACCCCTCTAGGATGTGCGGGAGTGTGCTGGGCGCTCACAGCCAGCCGGGCTGCC  
 ATTCAAGCAGAGCTCTGAGCAGGGAGGTGAAGAAAGGATGGCTCTGGGGCTGCAAGAGCTGGGACTTCATGTT  
 CTTCTAGAGAGGGCCACAAGAGGCCACAGGGTGGCCGGAGTTGTCAGCTGATGCCCTGCTGAGAGGCCAGGAAT  
 TGTGCCAGTGAGTGACAGTCATGAGGGAGTGCTCTCTGGGGAGGAAAGAAGGTAGAGCCTTCTGCTGAAAT  
 GAAAGGCCAAGGCTACAGTACAGGGCCCGCCCCAGCCAGGGTGTAAATGCCACGCTAGTGGAGGCTCTGGCAG  
 ATCCCTGCATTCCAAGGTCACTGGACTGTACGTTTATGGTGTGGAGGGTGGGTGGCTTAAAGAATTAAAGGGC  
 CTTGTTAGGCTTGGCAGGTAAAGAGGGCCAAGGTAAAGAACGAGGCCAACGGCACAAGCATCTATATATAAGT  
 GGCTCATTAGGTGTTATTTGTTCTATTAAAGAATTGTTTATTAAATTAAATAAAAATCTTGAAATCTC  
 TAAAA

175/615

**FIGURE 174**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSFPSHPKVHMDPNYCHPSTSLLHLCSSLAWSFTRLLHPPL  
SPGISQVVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESAFSSYSDLSEGEQEARFAAGVVAEQFAIAEAK  
LRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLGPHLQDLFTGHRFSPVRQGSVEPESDCSQTVSPDTLCSS  
LCSLEDGLLGSPARLASQLLGDELLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAAEEPAPCKDCQPL  
CPPLTGSGWERQRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**  
amino acids 1-15

**Casein kinase II phosphorylation site.**  
amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232, 285-289,  
324-328

**Tyrosine kinase phosphorylation site.**  
amino acids 44-52

**N-myristoylation site.**  
amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**  
amino acids 11-22

176/615

FIGURE 175

GGTTCCCTGGCGCTCTGTTACACAAGCAAGATAACGCCAGCCCCACCTAATTTGTTCCCTGGCACCCCTCCTGC  
TCAGTGCAGACATTGTACACTAACCCATCTGTTCTCTAAATGCACGACAGATTCCCTTCAGACAGGACAAC TG  
TGATATTCAGTTCTGATTGTAATAACCTCTAAAGCCTGAAGCTCTGTTACTAGCATTGTGAGCTTCAGTT  
CTTCATCTGAAAATGGGCATAATAACAAATCTATTCTTGCCACATCAAGGGATTGTTATTCCCTTAAAAAAAACC  
AATAACAAAGAAGCCTACAATGTGGCCTAGCAAAATTCTGTTCAACGTTGTTATTCACTCTATC  
GGGGAGCCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGCAGAAGTTTAAAACAATGGAAA  
TAAACCTATTCCTTGAAAGTGAAGCAAACCTAAACTCAGATAAGAAAATAACCAACCTCAAATCTAAGGC  
GAGTCATTCCCCTCCTTGAATCTACCCAAACACAGCCACGGAATAACAGATTCTCCAGTAACCATCAGCAGA  
GCATTCTTGGGCAGCTCAAACCCACATCTACCATTTCCACAAGCCCTCCCTGATCCATAGCTTGTCTAA  
AGTGCCTTGGAAATGCACCTATAGCAGATGAAGATCTTTGCCCCTCTCAGCACATCCCAATGCTACACCTGCTCT  
GTCTCAGAAAACCTCACTGGTCTTGGTCAATGACACCGTAAAACCTCTGATAACAGTCCATTACAGTTAG  
CATCCTCTCTCAGAACCAACTCTCCATCTGACCCCTTGATAGGAAACCAAGTGGATGGCTTACACAAA  
CAGTGATAGCTTCACTGGTTACCCCTTATCAAGAAAAACAACTCTACAGCCTACCTTAAATTACACCAATAA  
TTCAAAACTCTTCAAATACGTAGATCCCCAAAAGAAAATAGAAATAACAGGAATAGTATTCGGGCCATT  
AGGTGCTATTCTGGGTGTCATTGCTACTCTGTTGTCAGACAGAAAATGACAGGACTCTGCGATTAGACAATGCACCGAACCTTATGATGT  
TTCCCATCGCGACTTATGACGACAGAAAATGACAGGACTCTGCGATTAGACAATGCACCGAACCTTATGATGT  
GAGTTTGGAAATTCTAGCTACTACAATCCAACCTTGAAATGATTGACCCATGCCAGAAAAGTGAAAGAAAATGCACG  
TGATGGCATTCTATGGATGACATACTCCACTTCGACTCTGTATAGAACAAACAGCAAAAGGCCTAAAC  
GCAAGTGTCTACATCCACTAGCCTTGTACAAATTCTATTTCAAAGGTTACACAAAATTACTGTCACGTGG  
TTTGTCAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCATCCAAAGGTTTC  
TTTCTACAATTGGCCATCCTGAGGCATTACTAAGTAGCCTTAATTGTATTTAGTAGTATTTCTTAGT  
AGAAAATATTGTGGAATCAGATAAAACTAAAGATTTACCAATTACAGCCCTGCCTCATAACTAAATAAAAA  
ATTATTCCACCAAAAATTCTAAACAAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCTAAATT  
CAAGATTGCATTCTAAATGAAAATTGAAAGGGTGCTTTAAAGAAAATTGACTTAAAGCTAAAGAGGAA  
CATAGCCCAGAGTTCTGTTATTGGAAATTGAGGCAATAGAAATGACAGACCTGTATTCTAGTACGTTATAATT  
TTCTAGATCAGCACACACATGATCAGCCCACCTGAGTTATGAAAGCTGACAATGACTGCATTCAACGGGCCATGGC  
AGGAAAGCTGACCCCTACCCAGGAAAGTAATAAGCTTCTTAAAGTCTCAAAGGTTGGAAATTAACTTGT  
TTAATATCTAGGCTCAATTATTGGTGCCTTAAACACTCAATGAGAATCATGGT

177/615

**FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732  
><subunit 1 of 1, 334 aa, 1 stop  
><MW: 36294, pI: 4.98, NX(S/T): 13  
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENITTSNLKASHSPPL  
NLPPNNSHGITDFSSNSAEEHSLGSLKPTSTISTSPPLIHSFVSKVPWNAPIADEDLLPISAHPNATPALSSENFT  
WSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVEPSGWLTTSNDSFTGFTPYQEKTTLQPTLKFTNNSKLFPN  
TSDPQKENRNTGIVFGAILGAILGVSLLTIVGYLLCGKRKTDSFSHRRRLYDDRNEPVLRLDNAPEPYDVSFGNSS  
YYNPTLNDSAMPESEENARDGIPMDDIPPLRTSV

**Signal peptide:**  
amino acids 1-23

**Transmembrane domain:**  
amino acids 235-262

**N-glycosylation site.**  
amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159, 163-167, 218-222,  
225-229, 298-302, 307-311

178/615

**FIGURE 177**

ACCAAGGCATTGTATCTTCAGTTGTCATCAAGTCGAATCAGATTGGAAAAGCTCAACTTGAAGCTTCTGCCT  
GCAGTGAAGCAGAGAGATAGATATTATTACCGTAATAAAACATGGCTTCAACCTGACTTCCACCTTCCTA  
CAAATTCCGATTACTGTTGCTGTTGACTTGTCGCTGACAGTGGTGGGTGGGCCACAGTAACACTACTCGTGGG  
TGCCATTCAAGAGATTCTAAAGCAAGGAGTTCATGGCTAATTCCATAAGACCCCTCATTGGGGAAAGGGAAA  
AACTCTGACTAATGAAGCATCCACGAAGAAGGTTAGAACCTGACAACGTGCTCTGTGTCCTTACCTCAGAGG  
CCAGAGCAAGCTCATTCAAACAGATCTCACTTGGAAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGG  
CCGGTATCGCCCTCAGGAATGTAAGCTTACAGAGGGTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAACA  
CCTGATGTACCTGCTGGAACATCTGCATCCCTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCA  
CCAGGCTGAAGGTAAGGTTAATCGAGCAGAACTCTGAATGTTGGCTATCTAGAACGCTCAAGGAAGAAAA  
TTGGGACTGCTTATATTCCACGATGTGGACCTGGTACCGAGAATGACTTAACTTACAAGTGTGAGGAGCA  
TCCCAGGCATCTGGTGGTGGCAGGAACAGCACTGGGTAACGGTTACGTTACAGTGGATATTGGGGGTGTTAC  
TGCCCTAAGCAGAGAGCAGTTCAAGGTGAATGGATTCTCTAACAACTACTGGGATGGGAGGCGAAGACGA  
TGACCTCAGACTCAGGGTGAGCTCCAAGGAATGAAAATTCCCGGCCCTGCCTGAAGTGGTAAATATAACAT  
GGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTAACCAAGTGTACAGGT  
CTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTATATACAA  
CACAGTGGATTCTGGTTGGTGCATGACCTGGATCTTGGTGAATGTTGGAAGAACTGATTCTTGTGCA  
ATAATTGGCCTAGAGACTTCAAATAGTACACACATTAAGAACCTGTTACAGCTCATTGGTAGCTGAATT  
TCCTTTGTATTTCTTAGCAGAGCTCTGGTGAATGAGACTAAACAGTGTAAACAGCAGCTTCTTAG  
TCATTTGATCATGAGGGTTAAATATTGTAATATGGAACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGA  
AAAATGAACGCTATTGAGGACTCTGGTTGAAGGAGATTATTAATTGAAGTAATATATTGGATAAAA  
GGCCACAGGAATAAGACTGCTGAATGTCAGAGAACCCAGAGTTGTTCTGCTTCAAGGTAGAAAGGTACGAAGA  
TACAATACTGTTATTCAATTCTGTACAATCATCTGTGAAGTGGTGTGTCAGGTGAGAACGGCGTCCACAAAA  
GAGGGGAGAAAAGGCAGCAATCAGGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGC  
TGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGGTGTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCC  
CAGTGATGCCACAGAGAACATACATTCTCTATTAGTTTAAAGAGTTTGTAAAATGATTGTACAGTAGG  
ATATGAATTAGCAGTTACAAGTTACATATTAACTAATAAAATGTCTATCAAATACCTCTGTAGTAAAAT  
GTGAAAAGCAAAA

179/615

**FIGURE 178**

MGFNLTFHLSYKFRLLLLLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLIGKGKTLTNEASTKKVELD  
NCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPHRNREKHLMLLEHLHPFLQR  
QQLDYGIYVIHQAECKKFNRAKLNNVGYLEALKEENWDCFIFHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYR  
LRYSGYFGGVITALSREOFFKVNGFSNNYWGWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAE  
RMKLLHQVSERVWRTDGLLSSCSYKLVSVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**  
amino acids 1-27

**N-glycosylation sites.**  
amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**  
amino acids 191-202

180/615

FIGURE 179

CGTGGGCGGGGTGC CGCAGCGGGCTGTGGGCGGCCGGAGGAGCGACCGCCGAGTTCTGAGCTCCAGCTGC  
ATTCCCTCCCGTCCGCCACGCTCTCCCCTCCGGCCGAGGGTGGCCGAGGCTGTATGAACTAATCT  
CCGCATCCTCTGGCTTGCCCTCCGCCCTGGGCCCCGGCAGGGTGGCCGAGGCTGTATGAACTAATCT  
CACCAACCAGATAGCCCTGCCACCAACGGGAGCGGTGGTACCGATCTCGCCAGCCTGTGGCAAGGACAACGGCAG  
CCTGGCCCTGCCGCTGACGCCACCTCTACCGCTTCACGATCCACTGGACACACCCCGCTGGTGTACTGGCAAGGAT  
GGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTGGCCACGTGCCGGGGAAATCCCGGTCTCTGTCTGGTAC  
TGCCGCTGACTGCTGGATGTGCCAGCCTGTGCCAGGGGTTGTGGTCTCCCCATCACAGAGTTCCCTGTGGG  
GGACCTTGTGTACCCAGAACACTTCCCTACCCCTGGCCAGCTCCTATCTCACTAACAGCCCTGTGAAAGTCTC  
CTTCCTCCACGACCGAGCAACTTCCTCAAGACCGCCFTGTTCTCTACAGCTGGACTTCGGGACGGGAC  
CGAGATGGTACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGACCTCACCGTGAAGCTCAAAGT  
GGTGGCGGAGTGGGAAGAGGTGGAGGCCGATGCCACGAGGGCTGTGAAGCAGAAAGACCGGGACTCTCCGCCTC  
GCTGAAGCTGCAGGAAACCTTCAGGGCATCCAAGTGTGGGGCCACCCCTAACAGACCTCCAAAAGATGAC  
CGTGAACCTGAACCTCTGGGAGGCCCTCTGACTGTGTGGCCACGGTACAACCTGACCCACCTCAGGGACCTGGG  
GGAAGGGAGTGCCACCTGTGTCCTGGCCAGCACGGTACAACCTGACCCACCTCAGGGACCTGGG  
CTACTGCTTCAGCATCAGGGCAGAACATATCATCAGCAAGACACATCAGTACCAAGATCCAGGTGTGCCCTC  
CAGAACATCCAGCGGCTGTCTTGCTTCCATGTGCTACACTTATCAGTGTGATGTGGCCTCATCATGTACAT  
GACCCCTGCCGAATGCCACTCAGCAAAGGACATGGTGGAGAACCGGAGCCACCCCTGGGTCAGGTGTGCTG  
CCAGATGTGCTGTGGGCTTCTTGCTGGAGACTCCATCTGAGTACCTGGAAATTGTCGTGAGAACCCACGGGCT  
GCTCCCGCCCTCTATAAGTCTGCTAAACTACACCGTGTGA~~G~~CACTCCCCCTCCCCACCCATCTCAGTGT  
ACTGACTGCTGACTTGAGTTCCAGCAGGGTGGTGTGACCAACTGACCAAGGAGGGTCTATTGCGTGGGCTG  
TTGGCCTGGATCATCCATCTGACTGCTACAGTCAGCCACTGCCACAAGCCCTCCCTCTGTACCCCTGACCC  
CAGCCATTCAACCATCTGACTGAGTCCAGCCACTGACATAAGCCCACTCGGTTACCAACCCCTGACCCCTTAC  
TTGAAAGAGGGCTCTGCGAGGACTTGTGCTGGGGTGTCCATTGGGCTCTGACTCCTAGGTGGGCTGGCTGCCAC  
TGCCCATTCCCTCTCATATTGGCACATCTGCTGCTCCATTGGGGTCTCAGTTCTCCAGACAGCCCTACCT  
GTGCCAGAGAGCTAGAAAGGTATCAAAGGGTAAAGGTATAACATGACATAAGGGTGTACACATAGATGGGCACA  
CTCACAGAGAGAAGTGTGATGTACACACACACACACACACACAGAACATATAAACACATG  
CGTCACATGGGCAATTTCAGATGATCAGCTCTGTATCTGGTTAACGCGTTGCTGGGATGCACCCCTGCACTAGAGC  
TGAAAGGAAATTGACCTCAAGCAGCCCTGACAGGTTCTGGGCCGGCCCTCCCTTGTGCTTTGTCTCTGCA  
GTTCTGCGCCCTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGCAGGACTAAC  
TGAGTGTGAGAGTGCTTTATAAAATCACCTTATTGTGAAACCCATCTGAAACTTCACTGAGGAAA  
AGGCCTTGCAGCGGTAGAAGAGGTGACTCAAGGCCGGCGCGGTGGCTACGCTGTAATCCAGCACTTGGG  
AGGCCAGGGCGGGTGGATCACGAGATCAGGAGATCGAGACCAACCTGGCTAACACGGTGAACACCCGCTCTACT  
AAAAAAATACAAAAAAGTTAGCCGGGCGTGGTGGTGGCTGCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGA  
GAATGGTGCAGACCCGGAGGCGGAGCTGCACTGAGCCAGATGGGCCACTGCACTCCAGCCTGAGTGA  
GCGAGACTCTGCTCCA

181/615

**FIGURE 180**

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSIALPADAHILYRFHWI  
HTPLVLTGKMEKGLSSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGFVVLPIFEFLVGDLVVTQNTSLPWPSS  
YLTKTQLKVSFLLHDPSNFLKTALFLYSWDFGDGTQMVTEDSVVYYNYSIIGTFTVKLKVVAEWEVEPDATRAV  
KQKTGDFSASLKLQETLRGIQVLGPTLIQTFQKMTVTLNFLGSPPITVCWRLKPECLPLEEGECHPVSVASTAYN  
LTHTFRDPGDYCFSIRAENIISKTHQYHKIQVWPSRIQPAVFATPCATLITVMLAFIMYMTLRNATQQKDMVENP  
EPPSGVRCCCQMCQCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

**Important features of the protein:**

**Signal peptide:**  
amino acids 1-24

**Transmembrane domain:**  
amino acids 339-362

**N-glycosylation sites.**  
amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

182/615

FIGURE 181

CGGACGCGTGGCGGGCTCGGAACCTCCGTGGAGGGCCGGTGGGCCCTCGGCCTGACAGATGGCAGTGGC  
CACTGCGGGCGCAGTACTGGCCGTCTGGCGGGCGCTGTGGCTGGCGGCCGCCGGTCTGGCTGGGCCAGGGT  
CCAGCGGCTGCGCAGAGGCGGGACCCGCCCTATGCAAGGGAAAGACTGTGCTGATCACGGGGCGAACAGCG  
CCTGGGCCGCGCCACGGCCGCCAGCTACTGCGCTGGAGCGCGGGTGTATGGCTGCCGGGACCGCGCG  
CGCCGAGGAGGCGGGCTAGCTCCGCCGAGCTCCGCCAGGCCGGAGTGCGGCCAGAGCCTGGCGTCAG  
CGGGGTGGCGAGCTCATAGTCCGGAGCTGGACCTCGCCTCGCTGCCCTCGTGCCTGCCAGGGAAAT  
GCTCCAGGAAGAGCCTAGGCTGGATGTCTTGTATCAATAACGCAGGGATCTTCCAGTGCCCTAACATGAAGACTGA  
AGATGGGTTGAGATGCAAGTCCAGTGGAGTGAACCATCTGGGCACTTCTACTCACCAATCTCTCCTTGGACTCCT  
CAAAAGTTCAGCTCCAGCAGGATTGTTCTCCAAACTTATAAATAACGGAGACATCAATTGATGA  
CTTGAACAGTGAACAAAGCTATAATAAAAGCTTTGTTATAGCCGGAGCAAACACTGGCTAACATTCTTTTACCAAG  
GGAACTAGCCCGCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCTGGTATTGTACGGACAAATCT  
GGGAGGCACATACACATTCCACTGTTGGTCAAACCAACTCTCAATTGGTGTCAATGGCTTTTCAAAACTCC  
AGTAGAAGGTGCCAGACTTCCATTATTGGCCTCTCACCTGAGGTAGAAGGAGTGTCAAGGAAGATACTTGG  
GGATTGTAAAGAGGAAGAACTGTTGCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTGGGATATCAGTGA  
AGTGTGTTGGCTGCTAAATAGGAACAAGGAGTAAAGAGCTGTTATAAAACTGCATATCAGTTATATCTG  
TGATCAGGAATGGTGGATTGAGAACCTGTTACTGAAAGAAAAGAATTGGATATTGGAATAGCCTGCTAAGA  
GGTACATGTGGTATTGGAGTTACTGAAAATTATTGGATAAGAGAATTCAAGCAAGATGTTAAAT  
ATATATAGTAAGTATAATGAATAAAAGTACAATGAAAATACAATTATATTGTAAGGAAATTATAACTGGCAAGCA  
TGGATGACATATTAATATTGTCAGAATTAAAGTGAATGACTCAAAGTGTATCGAGAGGTTTCAAGTATTTGAGT  
TTCATGGCAAAGTGTAACTAGTTACTACAATGTTGGTGTGAAATTATCTGCCTGGTGTGCA  
CACAAGTCTTACTGGATAAAATTACTGGTAC

183/615

**FIGURE 182**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747
<subunit 1 of 1, 336 aa, 1 stop
<MW: 36865, pI: 9.15, NX(S/T): 2
MAVATAAAVLAALGGALWIAARRFVGPRVQLRRGGDPGLMHGKTVLITGANGLGRATAAELLRLGARVIMGCR
DRARAEAAAGQLRRELQRQAAECGPEPGVSGVGELIVRELDLTLASLRVRAFCQEMLQEEPRLDVLIINNAGIFQCPY
MKTEDGFEMQFGVNHLGHFLLTNLLGLLKSSAPSRIVVSSKLYKGDIINFDDLNSEQSYNKSFCYSRSKLANI
IFTRELARRLEGTVNVNLHPGIVRTNLGRHIHPIPLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSG
RYFGDCKEEELLPKAMDESVARKLWDISEVMVGLLK
```

**Important features:**

**Signal peptide:**

amino acids 1-21

**Short-chain alcohol dehydrogenase family protein**  
amino acids 134-144, 44-56 and 239-248

**N-glycosylation site.**

amino acids 212-215 and 239-242

184/615

**FIGURE 183**

AACAGGGATCTCCTTGCAGTCAGCCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGCAGCCGAAGATTCACTATGGTGAAGAAACTCTGAGCCGCACGGTCAGAACTCAGATACTGACCGCAAGGAGCTCCGAGTTGCCACCCAGAAAAAGAGGGCTCTGGGGAGATGTATGCTTACTCTTAGGCCCTTCATTCATCTTGCAAGGACTTATTGTTGGTGGAGCTGCATTTACAAGTACTCATGCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTGATTCTGAGGATCTGCAAATTCCCTCGTGGAGGAGAGCCTAACCTCCTGCCTGTGACTGAGGAGGCTGACATTGAGGATGACAACATTGCAATCATTGATGTGCCCTGCCCCAGTTCTCTGATAGTGACCCCTGCAGCAATTATTATCATGACTTGAAGAGGAATGACTGCTTACCTGGACTTGTGCTGGGAAC TGCTATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAATCTGGTAGAGCTTTGGCAAAC TGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTCAGAACGACCTA GTTGCCTGGAGGAATTCTGTGATGTTAGTAACCTTGGCATCTTATTACCAACTTTGCAATAACAGAAAGTCC TTCCGCCTCGTCGAGAGACCTTGTGCTGGTTCAACAAACGTGCCATTGATAATGCTGGAAGATTAGACAC TTCCCCAACGAATTATTATTGAGACCAAGATCTGCAAGAGTAAGAGGCAACAGATAGAGTGCTTGGTAATA AGAAGTCAGAGATTACAATATGACTTTAACATTAAAGGTTATGGGATACTCAAGATATTIACATGCATTAC TCTATTGCTTATGCTTAAAGGAAAAAAAGGAAAAAAACTAACTAACCACTGCAAGCTCTGTCAAATTAGTT TAATTGGCATTGCTTGGTTGAAACTGAAATTACATGAGTTCATTTTCTTGCAATTAGGGTTAGAT TTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAAATTCCATCGTTGTTTTGTTGTTGT TTTTCTTCCCTTAAGCTCTTATTACATCTTATGGTGGAGCAATTAAAATTGAAATTATTAAATT GTTTTGAACCTTTGTGTAAAATATATCAGATCTCAACATTGTTGGTTCTTTGTTTCATTGTACAAC TTCTGAAATTAGAAATTACATCTTGAGTTCTGTTAGGTGCTCTGTAATTAAACCTGACTTATATGTGAACAATT TTGAGACAGTCATTAAACTAATGCAGTGATTCTTCTCACTACTATCTGATTGTGGAATGCACAAAAT TGTGTAGGTGCTGAATGCTGTAAGGAGTTAGGTTGATGAATTCTACAACCCATAATAAAATTACTCTATAC AAAAAAAAAAAAAAAA

185/615

FIGURE 184

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828  
<subunit 1 of 1, 263 aa, 1 stop  
<MW: 29741, pI: 5.74, NX(S/T): 1  
MVKIAFNTPTAVQKEEARQDVALLSRTVRTQILTGKEILRVATQEKEGGSSGRCMLLGLSFILAGLIVGGACIY  
KYFMPKSTIYRGEMCFDSEDPANSLRGGEPNFLPVTEEADIREDDNIAIIDVPVPSFSDSPAAIIHDFEKGMT  
AYLDLLLGNCLMPLNTSIVMPPKNLVELFGKLASGRYLPQTYVVREDLVAVEEIRDVSNLGIFIFYQLCNNRKSFR  
RLRRRDLLLGFNKRайдKCWKIRHFPNEFIVETKICQE

Type II transmembrane domain:  
amino acids 53-75

N-glycosylation site.  
amino acids 166-170

Casein kinase II phosphorylation site.  
amino acids 35-39, 132-136, 134-138

N-myristoylation site.  
amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.  
amino acids 63-74

186/615

**FIGURE 185**

187/615

**FIGURE 186**

MALSSQIWAACLLLLLLASLTGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRDTHFPICIFCCGCCHR  
SKCGMCCKT

188/615

FIGURE 187

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTGTTCTAGGGAGGCAGGTGCTGGCCTGGATCTTCCAC  
**CATGTTCC**TGTTGCTGCCTTTGATAGCCTGATTGTCACCTCTGGCATCTCCCTGACTGCTCTCACCC  
CCTCTCGTTTCACTCATAGTGCAGCCATTGGAGCTCCTTGATCGCAAACCTACATGAAAAGCT  
GTTAAAAATCTTGCCTGGGCTACCTTGAGAATGGAGCAGGAGCCAAGGAGAAGAACCCAGCTTACAAGCC  
CTACACCAACGGAATCATTGCAAAGGATCCCACCTCACTAGAAGAAGAGATCAAAGAGATTCGTCGAAGTGGTAG  
TAGTAAGGCTCTGGACAACACTCCAGAGTTGAGCTCTGACATTCTACTTTGCGGAAAGGAATGGAGAC  
CATTATGGATGATGAGGTGACAAGAGATTCTCAGCAGAAGAAGTGGAGTCTGGAACCTGCTGAGCAGAACCAA  
TTATAACTCCAGTACATCAGCCTCGGCTCACGGTCTGTGGGGTAGGAGTGTGATTGGTACTGCTTCT  
GCTGCCGCTCAGGATAAGCACTGGCTTCACAGGGATTAGCCTCTGGTGGCACAACGTGGTGGGATACTT  
GCCAAATGGGAGTTAAGGAATCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCAGCGCT  
GACAGCCATCATCACCTACCATGACAGGGAAACAGACAAAGAAATGGTGGCATCTGTTGGCAATCATACCTC  
ACCGATCGATGTGATCATCTGGCCAGCGATGGCTATTAGCCATGGTGGGTAAGTGACGGGACTCATGGG  
TGTGATTCAAGAGGCCATGGTGAAGGCCATGCCACAGCTCTGGTTGAGCGCTCGGAAGTGAAGGATGCCACCT  
GGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAAGCAAGCTGCTATCCATCTTCCAGAAGAACCTG  
CATCAATAATACATCGGTGATGATGTTCAAAAAGGGAGTTGAATTGGAGCCACAGTTACCCGTTGCTAT  
CAAGTATGACCCCTCAATTGGCGATGCCCTCGGAACAGCAGAAATACGGGATGGTGAACGTAACCTGCTGCGAAT  
GATGACCAGCTGGGCCATTGTCTCAGCGTGTGGTACCTGCCCTCATGACTAGAGAGGCAAGATGAAGATGCTGT  
CCAGTTGCAATAGGGTGAATCTGCCATTGCCAGGGAGGACTTGTGGACCTGCTGTGGATGGGGCCT  
GAAGAGGGAGAAGGTGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGAACCA  
CAAGGACAGGAGCCGCTCCTGAGCCTGCCCTCCAGCTGGTGGGGCACCCTGCGGGGTGCCAACGGCTCAGAGC  
TGGAGTTGCCGCCGCCGCCCCACTGCTGTGCTCTTCCAGACTCCAGGCTCCCCGGCTGCTCTGGATCCCAG  
GACTCCGGCTTTCGCCAGCCGACGGGATCCCTGTGACCCGGCGCAGCCTACCCCTGGTGGCTAAACGGAT  
GCTGCTGGGTGTTGCGACCCAGGACGAGATGCCCTGTTCTTACAATAAGTGTGGAGGAATGCCATTAAAG  
TGAACTCCCCACCTTGCACGCTGTGGGGCTGAGTGGTTGGGGAGATGTGGCATGGTCTGTGCTAGAGATGG  
CGGTACAAGAGTGTATGCAAGCCCCTGTCAGGGATGTGCTGGGGGCCACCCGCTCTCCAGGAAAGGC  
ACAGCTGAGGCACTGTGGCTGGCTCGGCCCTAACATGCCCTTGGAGCTCTGCAAGACATGATAGGAAG  
GAAACTGTCATCTGCAAGGGCTTICAGAAAATGAAGGGTAGATTGCTGCTGTGATGGGTACTAAA  
GGGAGGGGAAGAGGCCAGGTGGCCGCTGACTGGGCCATGGGGAGAACGTGTGCTGACTCCAGGCTAACCTG  
AACTCCCCATGTGATGCGCGCTTGTGAATGTGTCTCGGTTCCCATCTGTAATATGAGTCGGGGGAATG  
GTGGTGAATTCTACCTCACAGGGCTGTGTGGGATTAAAGTGTGCGGGTGAGTGAAGGACACATCACGTTCA  
TGTTCAAGTACAGGCCACAAAACGGGCACGGCAGGCAGGCTGAGCTCAGAGCTGCTGCACTGGCTTGATTG  
TTCTGTGAGTAAATAACTGGCTGGTGAATGA

189/615

FIGURE 188

MFLLLPFDLSLIVNLLGISLTVLFTLLLVLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRMERGAKENHQLYKP  
YTNGIIAKDPTSLEEEIKEIIRRSGSSKALDNTPEFELSDIFYFCRKGMETIMDDEVTKRFSAEELSWNLLSRTN  
YNFQYISLRLTVLWGLGVLIACYCFLPLRIALAFTGISLLVVGTTVGYLPGNGRFKEFMSKHVHLMCYRICVRAL  
TAIITYHDRENPRNGGICVANHTSPIDVIIASDGYYAMVGQVHGGLMGVIORAMVKACPHVWFERSEVKDRHL  
VAKRLTEHVQDKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTLRM  
MTSWAIVCSVWYLPPMTREADEDAVQFANRVKSAIARQGLVDLLWDGLKREKVKTDFKEEQQKLYSKMIVGNH  
KDRSR

190/615

FIGURE 189

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCGGACCCCTGGCCCTCACGTCTCCTCCAGG  
GATGGCGCTGGCGGCTTGATGATGCCCTCGGCAGCCTCGGCACACCTGGCAGGCCAGGCTGTCCCAC  
CATCCTGCCCTGGGCTGGCTCCAGACACCTTGACCGATAACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAA  
GGCAGCCCCCTGCTAAAGGAGGAAATGGCCACCATGCCCTGCTCGGGAAATCTGGGAGGCAGCCCAGGAGAC  
CTGGGAGGACAAGCGTCGAGGGCTTACCTTGCCCCCTGGCTCAAAGCCCAGAATGGAATAGCATTATGGTCTA  
CACCAACTCATCGAACACCTTGACTGGAGTTGAATCAGGCCGTGCGGACGGGCGGAGGCTCCGGAGCTCTA  
CATGAGGGACTTCCCTCAAGGCCCTGCATTCTACCTGATCCGGCCCTGCAGCTGCGAGGCAGTGGGGG  
CTGCAGCAGGGGACCTGGGAGGTGGTGTCCGAGGTGTGGGAGCCTTCGCTTGAAACCAAGAGGCTGGGGGA  
CTCTGTCGGCTTGGCCAGTTGCCCTGGCTCCAGCTCCAGATAAGGCAGTGGCCACAGATTGGGAGAAGAGGCG  
GGGCTGTGTCTCGGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCTCTGCCCCCTGGAAGAC  
TCTGCTCTGGCCCTGGAGAGTCCAGCTCAGGGGTTGGGCTTGAAAGTCCAACATCTGCCACTTAGGAGC  
CCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAGCAGCCTTGAGAAGCAAGAACATGGTCCGGAC  
CCAGCCCTAGCAGCCTCTCCCCAACCAAGGATGTTGCCCTGGGAGGCCACAGCAGGGCTGAGGGAACTCTGCTA  
TGTGATGGGACTTCTGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGA  
GACATGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

191/615

FIGURE 190

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHALLRESWEAAQET  
WEDKRRGLTLPPGFKAQNIGIAIMVTNSSNTLYWELNQAVRTGGGSRELYMRHFFKALHFYLIRALQLLRGSGG  
CSRGPGVVFRGVGSLRFEPKRLGDSVRLGQFASSSLDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKT  
LLLAPGEFQLSGVGP

192/615

FIGURE 191

GTGGCTTCATTCAGTGGCTGACTTCCAGAGAGCAATATGGCAGTTCCCCAACATGCCTCACCCCTCATCTATAT  
CCTTTGGCAGCTCACAGGGTCAGCAGCCTGGACCGTGAAAGAGCTGGTCGGTCCGTTGGTGGGGCGTGAC  
TTTCCCCCTGAAGTCAAAGTAAGCAAGTGAATCTATTGTCTGGACCTCAACACAACCCCTTTGTCAACCAT  
ACAGCCAGAAGGGGGCACTATCATAGTACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTA  
CTCCCTGAAGCTCAGCAAACGTAGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATAACAGCTCATCACTCCA  
GCAGCCCTCCACCCAGGAGTACGTGCTGCATGTACGAGCACCTGCAAAGCTAAAGTCACCATGGGTCTGCA  
GAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTATAC  
CTGGAAGGCCCTGGGCAAGCAGCAATGAGTCCCATAATGGGTCCATCTCCCCATCTCCTGGAGATGGGAGA  
AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAGCAGAAACTTCTCAAGCCCCATCCTGCCAGGAA  
GCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCTGTGTCTCTGTTGGTGCCTCTGCT  
CAGTCTCTTGACTGGGCTATTCTTGGTTCTGAAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAA  
GAGAGTGGACATTGTGGGAAACTCTAACATATGCCCTTACTCTGGAGAGAACACAGAGTACGACACAATCCC  
TCACACTAATAGAACAACTCTAACAGAACAGATCCAGCAAATACGGTTACTCCACTGTGAAATACCGAAAAAGAT  
GAAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAGAATGTTATCTAGACAGC  
AGTGCACCTCCCTAACGTCTGCTCA

193/615

**FIGURE 192**

MAGSPTCLTLIYILWQLTGSAAASGPVKELVGSGGAVTFPLKSKVQVDSIVWTFNTTPLVTIQPEGGTIIIVTQN  
RNRERVDFFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQPSTQEYVLHVEHLSKPVMTMGLQSNKNGTCVTNLT  
CCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESSDMTFICVARNPVSRFSSPILARKLCEGAADDPDSS  
MVLLCLLLVPLLLSPVLGLFLKRERQEEYIEEKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA  
NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI

194/615

**FIGURE 193**

GGAGGAGGGAGGGCGGGCAGGCCAGCCCAGAGCAGCCCCGGGACCCAGCAGGACTCTCTTCCAGCCCAGG  
TGCCCCCACTCTCGCTCCATTGGCGGGAGCACCCAGTCTGTACGCCAAGGAACCTGGTCTGGGGCACC**ATG**  
GTTTCGGCGCAGCCCCAGCCTCCTCATCCTCTGTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCGC  
TCTGTGCCCTGAAGGCCACGTCCCTGGAGGATGTGGGGTAGTGGGGAGGGCAGGGCTGTCGGGCTCCTCC  
CCGAGCCTCCGCCACCCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCCCTGGGGC  
CCATCACCCCCCACCACCTCCTGGATGGGATAGTGGACTCTCGCCAGTACGTGATGCTGATTGCTGTGGT  
GGCTCCCTGGCTTCTGCTGATGTTCATCGTCTGTGCCCGGTGATCACCCGGCAGAAGCAGAAGGCCTGGCC  
TATTACCCATCGTCCCTCCCCAAGAAGAAGTACGTGGACCAAGAGTGAACGGGGGGGGGGGGGGGGGGGG  
GAGGTCCCCGACAGAGCCCCGACAGCAGGGCCGAGGAAGGCCCTGGATTCCCTCCGGCAGCTCCAGGGCAGACATC  
TTGGCCGCCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGCGGTGGGACGGCAGGGATGGTGGAG  
GGCAGGGGGCGCAGAGGAAGAGGAAGGGCAGCCAGGGGGACAGGAAGTCCAGGGACATGGGGTCCCAGTG  
GAGACACCAAGGGCAGAGGGAGGGCTGCTCAGGGGCTCTGAGGGGGCTGTGGTGGGGTGAAGGGCCAAGGG  
GAGCTGGAAGGGTCTCTTGTAGCCCAGGAAGGCCAGGACAGTGGGTCCCCCGAAAGGCCCTGTGCTTGC  
AGCAGTGTGTCACCCAGTGT**C****TAA**CAGTCCTCCCGGGCTGCCAGCCCTGACTGTCGGGCCCCAAGTGGTCACCT  
CCCCGTGTATGAAAAGGCCCTGACTGCTTCCCTGACACTCCCTTGGGCTCCCTGTGGTGCACATCC  
CAGCATGTGCTGATTCTACAGCAGGGCAGAAATGCTGGTCCCCGGTGGGGGAGGAATCTACCAAGTGCACATCA  
TCCTTCACCTCAGCAGCCCCAAAGGGTACATCCTACAGCACAGCTCCCTGACAAAGTGAAGGGAGGGCACGT  
CCCTGTGACAGCCAGGATAAAACATCCCCAAAGTGTGGATTACAGGGGTGAGGCCACCGTGCCCGGGCAAAC  
TACTTTTAAACAGCTACAGGGTAAATCTGCAAGCACCCACTCTGGAAAATACTGCTCTTAATTTCCTGAAG  
GTGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGTATAGGGCATTAAATCTCTCAAGCGCTCTC  
CAAGCACCCCCGGCTGGGGTGAGTTCTACATCCGCTACTGCTGCTGGGATCAGGGTGAATGAATGGAACCT  
TCCTGTCTGGCCTCAAAGCAGCTAGAAGCTGAGGGCTGTGTTGAGGGGACCTCCACCCCTGGGAAGTCCGA  
GGGGCTGGGAAGGGTTCTGACGCCAGCCTGGAGCAGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGT  
CTGGCAGCTGTGTCACAATATTGTCAGTCCTCGACAGGGAGCCTGGGCTCCGTCTGCTTAGGGAGGCTCT  
GGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGCTCCCCAACCTCTGCACAGCTCCAGGTGCTGAGATA  
TAATGCACCAAGCACAATAACCTTATTCCGGCCTGAAAAAAAAAAAAAAAAAAAAAAAGA  
AAAAAAAAAAAAAAAGA

195/615

**FIGURE 194**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852  
><subunit 1 of 1, 283 aa, 1 stop  
><MW: 29191, pI: 4.52, NX(S/T): 0  
MVSAAAPSILLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGSSASSPSILPPPWTTPALSPTSMGPQPTTLG  
GPSPPPTNFDLGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKOKASAYYPSSFPKKKYVDQSDRAGGPRAF  
SEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSPTRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVAQGHGVP  
VETPEAQEEPCSGVLEGAVVAGEGQGELEGSLLLQAQEAQGPVGPPESPCACSSVHPSV

**Signal peptide:**  
amino acids 1-25

**Transmembrane domain:**  
amino acids 94-118

**N-myristoylation site.**  
amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199, 211-217, 238-244,  
242-248

196/615

FIGURE 195

GAAAGACGTGGTCTGACAGACAGACAATCCATTCCCTACCAAAATGAAGATGCTGCTGCTGCTGTTGGGA  
CTGACCCTAGTCTGTGTCATGCAGAAGAAGCTAGTTCTACGGGAAGGAACCTTAATGTAGAAAAGATAATGGG  
GAATGGCATACTATTATCCTGGCCTCTGACAAAAGAGAAAAGAGATAAGAACATGGCAACTTAGACTTTCTG  
GAGCAAATCCATGTCTGGAGAATTCTTAGTTCTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCGAATT  
TCTATGGTGCTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATAACATTACTATA  
CCTAAGACAGACTATGATAACTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGAAACCTTCCAGCTGATG  
GGGCTCTATGCCGAGAACAGATTGAGTTCAAGACATCAAGGAAAGGTTGCACAACATATGTGAGGAGCATGGA  
ATCCTTAGAGAAAATCATGACCTATCCAATGCCAATCGCTGCCTCCAGGCCGAGAATGAAGAATGGCCTGA  
GCCTCCAGTGTGAGTGGACACTCTCACCAAGGACTCCACCATCATCCCTTCTATCCATACAGCATCCCCAGTA  
TAAATTCTGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACTAGGAT  
ACCTCATCAAGAATCAAAGACTCTTAAATTCTCTTGATACACCCCTTGACAATTTCATGAAATTATTCT  
CTTCTGTCAATAATGATTACCCCTGCACTAA

197/615

**FIGURE 196**

MKMLLLLCLGLTLVCVHAEFASSTGRNFNVEKINGEWTIILASDKREKIEEHGNFRLFLEQIHVLNSLVLKVH  
TVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLINEKDGETFQLMGLYGREPDLSSDIKE  
RFAQLCEEHGILRENIIDLDSNANRCLQARE

198/615

FIGURE 197

GGCTCGAGCGTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGGATGGACATCCTGCAATGGATTAGCCTG  
CTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACTCTAATTGTCAGCTTAGTTGAGGAAGACCAATT  
TCTCAAAACCCCACCTCTTGCTTGGAGTGGTCCCAGGAATTATAGGAGCAGGTCTGATGCCATCCAGCA  
ACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCACAAACAGAACTGGATGTTCTTCATCATTTTC  
AGTGTGATCACAGTCATTGGTCTGTATTGCATGCTGATATCCATCCAGGCTCTTAAAAGGTCCCTCATG  
TGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTCATTGAAAAACATCAGTGACATTCACTCAGAAC  
TTCAACTTGCACTGGTTTCAATGACTCTTGTGCACCTCCTACTGGTTCAATAAACCCACCAGTAACGACACC  
ATGGCGAGTGGCTGGAGAGCATCTAGTTCCACTTCGATTCTGAAGAAAACAACATAGGTTATCCACTCTCA  
GTATTAGGTCTATTGCTTGTGGAATTCTGGAGGTCTGTTGGGCTCAGTCAGATAGTCATCGGTTCT  
GGCTGTCGTGTGGAGTCTAAGCGAAGAAGTCAAATTGTGTAGTTAATGGGAATAAAATGTAAGTATCAGTA  
GTTTGAAAAAAAAAAA

199/615

**FIGURE 198**

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPATTMSLTARKR  
ACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDS  
CAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGLLLGVILEVLFGLSQIVIGFLGCLCGVSKRR  
SQIV

200/615

FIGURE 199

ATCCGTTCTTGCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGGTGAAGGAGCAGTG  
AGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAGATCCGTGGGCTGCAGACCCCC  
CGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTCGAACACTGTGACATGGAGAGAGTGACCTGGCCCTCTCCT  
ACTGGCAGGCCTGACTGCCTTGGAGCCAATGACCCATTGCCAATAAGACGATCCCTTCTACTATGACTGGAA  
AAACCTGCAGCTGAGCGGACTGATCTGGGAGGGCTCTGGCATTGCTGGGATCGCGGAGTTCTGAGTGGCAA  
ATGCAAATACAAGAGCAGCCAGAACGAGCACAGTCTGTACCTGAGAAGGCCATCCACTCATCACTCCAGGCTC  
TGCCACTACTTGTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACCTCCTC  
CCCTGGGAGGCCTTATCCTCAAGGAAGGACTCTCTCCAAGGGCAGGCTGTTAGGCCCTTCTGATCAGGAGGC  
TTCTTATGAATTAAACTCGCCCCACCACCCCTCA

201/615

**FIGURE 200**

MERVTLALLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGLLAIAGIAAVLSGKCKYKSSQHQHPVPE  
KAIPLITPGSATTC

202/615

**FIGURE 201**

203/615

**FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212  
><subunit 1 of 1, 440 aa, 1 stop  
><MW: 42208, pI: 6.36, NX(S/T): 1  
MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVSEALGQGT  
REAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVPGHSGAWETSGGHGI  
FGSQGGLGGQQGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGPPNFTNTQGAVAQPGYGSVRASNQ  
NEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGGSSGSSGGSSGGSSGNSGGS  
RGDSGSESSWGSSTGSSSGNHGGGGNGHKGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLLLGGS  
GDNYRGQGSSWGSGGDAVGGVNSETSPGMNFDTFWKNFKSKLGFINWDIAINKDQRSSRIP

**Signal peptide:**  
amino acids 1-21

**N-glycosylation site.**  
amino acids 265-269

**Glycosaminoglycan attachment site.**  
amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**  
amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**  
amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96,  
96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169,  
178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245,  
240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276,  
271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297,  
292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

**Cell attachment sequence.**  
amino acids 301-304

204/615

**FIGURE 203**

GGAGAAGAGGTTGTGGGACAAGCTGCCAGAGAAGGATGTCGCTGCTGACCTGCCCTGGCTGGCCTCA  
GACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGGTGTGGCTCCAGTGTTCACAGCCCCAAAACGAACTGGTTTGGG  
GGACCTATGCCCTATAACAACGCGCCGCTCCAGTGTTCACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCACCTATTCCCAGG  
GCTTACGGTATGGCTGGGTCCCACATCCCCCTCATCGTTTATGCCACCCCTGACACCACATCGGTCTATCACCA  
ATGCCTCAGCTGCCATTGACCCAGGATAATCTCTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATAC  
TGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCGCCCTCCATTCAACATCCTGAAGT  
CCTATATAACGATCTCAACAAGAGTCAAACATCATGCTTGACAAGTGGCAGCACCTGGCTCAGAGGGCAGCA  
GTCGTCTGGACATGTTGAGCACATCAGCCTCATGACCTGGACAGTCTACAGAAATGCATCTTCAGCTTGACA  
GCCATTGTCAGGAGAGGCCACTGAATATAGGCCACCATCTGGAGCTCAGTGCCCTTGAGAGAAAAGAACCC  
AGCATATCCTCCAGCACATGGACTTCTGTATTACCTCTCCCATGACGGGCGGCCCTCCACAGGGCTGCCGCC  
TGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGGCGTCGCACCCACTCAGGGTATTGATGATT  
TCAAAGACAAAGCCAAGTCAAAGACTTGGATTTCATGATGCTCTGCTGAGCAAGGATGAAGATGGAAAGG  
CATTGTCAGATGAGGATAAAGAGCAGAGGCTGACACCTCATGTTGGAGGCCATGACACCCAGGGCAGTGGCC  
TCTCCTGGGTCTGTACACCTTGGCAGGCACCCAGAATACCAGGAGCGCTGCCACAGGAGGTGCAAGAGCTTC  
TGAAGGACCCGATCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCCCTCCTGACCATGTGCGTGAAGG  
AGAGCCTGAGGTTACATCCCCAGCTCCCTCATCTCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCC  
GAGTCATCCCCAAAGGATTACCTGCCTCATCGATATTATAGGGGTCCATCACACCCAACTGTGTGGCCGGATC  
CTGAGGTCTACGACCCCTTCCGTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTATTCTTTCT  
CCGCAGGGCCCAGGAACGTACATGGCAGGCAGGCGTTCGCCATGGGGAGATGAAAGTGGCTCTGGCGTTGATGCTGC  
TGCACCTCCGGTTCTGCCAGACCAACTGAGCCCCGCAAGGAAGCTGGAATTGATCATGCGCCGAGGGCAGGATT  
TTGGCTGCCGGTGGAGCCCTGAATGTAGGCTTGCAGTGACTTCTGACCCATCCACCTGTTTTGCAGATT  
GTCATGAATAAAACGGTGCTGTCAAA

205/615

**FIGURE 204**

MSLLSLPWLGILRPVAMSPWLLLLVVGSWLLARILAWTYAFYNNCRLQCFQPPKRNWFHGHLGLITPTEEGLK  
DSTQMSATYSQGFTVWLGPPIIPFIVLCHPTIRSITNASAAIAPKDNLFIRFLKPWLGEGLLSGGDKWSRHRM  
LTPAFHFNILKSYTIFNKSANIMLDKWQHASEGSSRLDMFEHISLMTLDSIQKCIFSFDSHCQERPSEYIATI  
LELSALVEKRSQHILQHMDFLYLYLSHDGRFHACRLVHDFTDAVIREERRRTIPLTOGIDFFFKDKAKSKTLDFID  
VLLLSKDEDGKALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLRHPEYQERCRQEVAELLKDRDPKEIEWDDL  
AQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPPEVYDPFRFPENS  
KGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLNVGLQ

206/615

**FIGURE 205**

TCCCTTGACAGGTCTGGTGGCTGGTGGGGTCACTGAAGGCTGTCTTGATCAGGAAACTGAAGACTCTGTCT  
TTGCCACAGCAGTTCCTGCAGCTCCTGAGGTGTGAACCCACATCCCTGCCCCCAGGGCACCTGCAGGACGC  
CGACACCTACCCCTCAGCAGACGCCGGAGAGAAATGAGTAGCAACAAAGAGCAGCGGTAGCAGTGTCTGATC  
CTCTTGCCTCATCACCATCCTCATCCTCACAGCTAACAGTGCCTAGGCTTCCATTACGGCTCCCTG  
CGGGCCGTAGCCGCCACCTGTAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCTCCATTCTCGGCAAC  
AAGACACTGCCCTCTCGGTGCCACCAGTGTGTATTGTCAGCAGCTCCAGCCACCTGCTGGCACCAAGCTGGC  
CCTGAGATCGAGCGGGCTGAGTGACAATCCGATGAATGATGCACCCACCAGTGTACTCAGCTGATGTGGC  
AACAAAGACCACCTACCGCGTGTGGCCCATTCCAGTGTGTTCCGCGTGTGAGGAGGCCAGGAGTTGTCAAC  
CGGACCCCTGAAACCGTGTTCATCTCTGGGGCCCCGAGCAAGATGCAGAAAGCCCCAGGGCAGCCTCGTGC  
GTGATCCAGCGAGCGGGCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCCGATGCGGCAATT  
GACGACCTCTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATCGTGTGAGCACAGGCTGGTTACC  
ATGGTGATCGCGGTGAGTTGTGACCCAGTGCATGTCATGGCATGGTCCCCCCTAACACTGCAGCCAGCG  
CCCCGCTCCAGCGCATGCCCTACCAACTACGAGGCCAAGGGGGCGAGAATGTGTCACCTACATCCAGAAT  
GAGCACAGTCGAAGGGCAACCACCAGCCTCATCACCAGAAAAGGGTCTTCTCATCGTGGGGCCAGCTGTAT  
GGCATCACCTCTCCACCCCTCTGGACCTAGGCCACCCAGCCTGGGACCTAGGCTTGTGGAGTGTCTCCAG  
AGCCTCCGGCCAGCCGCTAGGCCAGGGACCATCTCTGCCAATCAAGGCTTGTGGAGTGTCTCCAG  
AGGGCTTGAGGAGGATGTATCTCCAGCCAATCAGGGCTGGGGATCTGTTGGCGAATCAGGGATTGGGAGT  
CTATGTGGTAATCAGGGGTGTCTTCTTGCAAGTGTCTGGCAGGCTGGCACAGTCATCAGGGTAGAGGGGTATT  
TCTGAGTCATCTGAGGCTAAGGACATGTCCTTCCATGAGGCTTGGTCAAGGAGCTGGGAACTGGGTGTTGCC  
AATCACTCCCCACTCTGCTGGATAATGGGGTCTGTCCAAGGAGCTGGGAACTGGGTGTTGCC  
CCAGCACCAAGAAAGAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCCGGCAGAGAATTGTGGGGTGTGG  
AGGITGTGGGGGGGGTGGGAGGTCCCAGAGGTGGGAGGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTTG  
GACAAACCCCTCCCCCTCTGGCACCCCTCTGCCACACCAGTTCCAGTGGAGTCTGAGACCCCTTCCAC  
CTCCCCCTACAAGTGCCCTCGGGCTGTCTGCCCTCCGCTGGACCCCTCCAGCCACTATCCCTGCTGGAGGCTCA  
GCTCTTGGGGGTCTGGGTGACCTCCCCACCTGAAACTTGGGTATTTGCCAAACTCTTCAG  
GTTGGGGACTCTGAAGGAAACGGGACAAACCTTAAGCTGTTCTAGGCCAGCTGCCATTAGCT  
GGCTCTTAAAGGGCCAGGCCTCTTTCTGCCCTCTAGCAGGGAGGTTTCCAAGTGTGGAGGCCCTTGGGG  
CTGCCCTTGCTGGAGTCAGTGGGGCTTCCGAGGGTCTCCCTGACCCCTGTGCTCTGGGATGGCTGTG  
GGAGCTGTATCACCTGGGTCTGTCCCCCTGGCTGTATCAGGCACATTAAAGCTGGCCCTAGGGGTGT  
GTTTGTCTCCTGCTCTGGAGCCTGGAAGGAAAGGGCTCAGGAGGAGGCTGTGAGGCTGGAGGGACAGATG  
GAGGAGGCCAGCAGCTAGCCATTGCACACTGGGTGATGGTGGGGCGGTGACTGCCAGACTGGTTGT  
ATGATTTGTACAGGAATAAACACACCTACGCTCCGGAAAAAAAAAAAAAA

207/615

**FIGURE 206**

MSSNKEQRSAVFVILFALITILILYSSNSANEVFHYGSRLGRSRRPVNLKKWSITDGYVPILGNKTLPSRCHQCV  
IVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRVLRRPQE VNRTPETVFIGWG  
PPSKMOKPQGSLSLVRVIQRAGLVFPNMEAYAVSPGRMRQFDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHV  
HVVGMVPPNYCSQRPRLQRMPYHYYEPKGDPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

**Signal peptide:**  
amino acids 1-29

**Transmembrane domain:**  
amino acids 9-31 (type II)

**N-glycosylation site.**  
amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 50-54

**Casein kinase II phosphorylation site.**  
amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**  
amino acids 253-262

**N-myristoylation site.**  
amino acids 37-43, 114-120, 290-294

208/615

FIGURE 207

GTAGCGCGCTTGGGCTCCGGCTGCCGCTGCCGCCGCCCTGGGCGTGGAGGCCAGGAGCAGTCAC  
CGCCATGGCAGGCATCAAAGCTTGATTAGTTGCTTGGAGGAGCAATCGGACTGATGTTTGATGCTTGG  
ATGTGCCCTTCCAATATAACAACAAATACTGGCCCTCTTGTCTATTTCATCCTTCACCTATTCCATA  
CTGCATAGCAAGAAGATTAGTGGATGATAAGATGCTAGAGTAACGCTTGTAAAGGAACATGCCATCTTCTTAC  
AACGGGCATTGCGTGCAGCTTGGACTCCCTATTGTATTGCGAGACATCTGATTGAGTGGGGAGCTTG  
TGCACCTGTTCTCACAGGAAACACAGTCATCTTGCACACTATACTAGGCTTTCTGGCTTGGAAAGCAATGA  
CGACTTCAGCTGGCAGCAGTGGT~~GAAAAGAA~~ATTACTGAACATATTGCTAAATGGACTTCCTGTCAATTGTTGGCC  
ATTCAACGACACAGGAGATGGGCAGTTAATGCTGAATGGTATAGAAGCCTTGGGGTATTAGGTGCTCC  
CTTCTCACTTTATTGTAAGCATACTATTTCACAGAGACTTGCTGAAGGATAAAAGGATTTCTTTGGAA  
AAGCTTGACTGATTCACACTATCTATAGTATGCTTTGTGGTCTGCTGAATTAAATATTIATGTGTTT  
TTCTGTTAGGTTGATTGTTGGAAATCAATATGCAATGTTAAACACTTTTAATGTAATCATTTGCAATTGGT  
TAGGAATTCAAATTCGCCGGCTCTTACTGGTCAGTACATCTTCTCTAAATTAGCTTCCATT  
TTACAAAAAATTAAAAAATAGGTTTCACTGGTCAAGGATGACATCACTCCCAATGTTAGCAGACATACAGAC  
GGTGGCATACGTTAGACTGATACTCAGTCAAATAGCTGATTTACCTCAGAGGGCCAAGTGTAA  
TGCCCATGCCCTCCGTTAAGGGTTGTTGTTACTGGTAGACAGATGTTGTGGATTGAAAATTATTATGG  
AATTGCTACAGAGGAGTGTCTTCTCAATTGTTAGAAGAATTATGTTAAACTTTAAGGTAAAGGGTGTAAA  
ACATTGGAGATAAGGTTTATTATGTTATTAGGTTAGAGTGAGTTGCAATGTGGAAAGAAATGACATTG  
AAATTCCAGTTTGAATCTGTTCTATTATAAGTGAATTTGTGATCTCTATCAACCTTCATGTTTACC  
CTGTTAAAATGGACATACATGGAACCAACTACTGATGAGGGACAGTTGTATGTTGCAATATGCCAGAAAAC  
CTTCCCTGCTTCCCTTGTACTTACCTGAAATAATTGCTATGCCGTACATCAGAGTGCCCCCTCCCTGCA  
AGGCCTTCCCATGATTAACAGTAACTGTTAGCTTACAGATAATTGCAATTACAGTTAAGATTTAGAC  
ATGGTAATGTTAGCTTCTAAGGTTATATGTAATTAAAGTATTGTTAAAGACAAGTTCCTGT  
ATACCTGTAACGTTGATTGAGTTGATCATGATAGATCTGCTGTTCTTATGAAAGTTATTCTCAAGAAAATG  
GAGTTAATGCAAAGTAGCCAAGTCCAGCTATAGCAGCTTCAAAACATACCTGACCAAAAAATTCCAGTAAAC  
CAGGCATGATCAATTATAGTGGTCGTTACATCTAATAATTACAGGACTTTTCAGGAGTGGGTTATAAAA  
CATTCAAGTGGCTGACAGTATTGTTAGGATATTGTTGTATGTTTATTCACTATACTTACATAAAAATT  
ATTCGCCATCAGCCAAAACCTAGTAATCATGACAGCTGCTGTTGTTTATGAAAGTTATTCTCAAGAAAATG  
GGAATAAAATTGGGATTGTTAGCTTTACTAAAGATGCCAAAGCCACAGGTTTATGCTTAACCTAAGC  
CATGACTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCGCGTGTGGCTGGAGCCCTCCACTGGAGGC  
TGAAAGTGGCTTGTGGTATTATAATGTTCAAGAGGAAGGTGCAGGTACACATGAGTTAGAGAGCTGGT  
GAGACAGTTGGGAAACTCTTGTGCTGTTGACTGACTGGACTTTTGTGAGGAAGTGCAATTCTGTCCTTC  
CCTATTCTGTTCTGGATGTCAGTGCAGTGCACTGCTACTGTTTATCCACTTGGCCACAGACTTTCTAACA  
GCTGCGTATTATTCTATACTAATTGCAATTGGCAGCATTGTCCTTGACCTTGTATAACTAGCTTGCACATAGT  
GCTGTCCTGATTCTAGGCTAGTTACTTGAGATATGAAATTTCATAGAATATGCACTGATAACACATTACCAT  
TCTTCTATGGAAAGAAAATTGGATGAAACAATAAGATTAAATATCTATTAAAAAA

209/615

**FIGURE 208**

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAMSACKELAIFLTT  
GIVVSAFGLPIVFARAHLIEWGACALVLTGNTVIFATILGFFLVFGSNDDFSWQQW

210/615

**FIGURE 209**

CTTGCAGAGAAAGACTTTGTGCAGCACCCCTTAAAGGGTGA~~T~~CGTCCCAC~~T~~GTGTTCTCTCCTGGTGC  
AGAGTTGCAAGCAAGTTATCAGAGTATGCCA~~T~~GAAGTTGTC~~C~~CCCTGCC~~T~~GCTGGTGA~~C~~CTTG~~C~~CTGCC  
TGGGGACTTGGGT~~C~~AGGCCCGAGGCAAAGCAAGGAAGCA~~T~~GGGGAGGAATTCCATTCCAGACTGGAGGGA  
GAGATTCTGCACTATGCGTCCCAGCAGCTTGGGCAAGGTGCTGGAGAAGTCTGGCTTCGCGTCGACTGCCGCA  
ACACAGACCAGACCTACTGGTGTGAGTACAGGGGCAGCCCAGCATGTGCCAGGCTTTGCTGCTGACCCAAAC  
CTTACTGGAATCAAGC~~O~~CTGCAGGAGCTGAGGCC~~T~~ACCATGCGTGCCAGGGGCCGGTGC~~T~~AGGCCAT  
CCGTGTGCAGGGAGGTGGACCCCAGGCCATATGCAGCAGGTGACTTCCAGCCTCAAGGGCAGCCCAGGCCA  
ACCAGCAGCCTGAGGTGGACGCCATCTGAGGCCAACAGTGA~~A~~ACTCACAGAAGCAACACAGCTGG  
GAAAGGACTCGATGGAAGAGCTGGAAAAGCCAACCCACCACCCGACCCACAGCCAACCTACCCAGCCTGGAC  
CCAGGCCGGAGGGAATGAGGAAGCAAAGAAGAAGGCC~~T~~GGGAACATTGTTGAAACCC~~T~~CCAGGCC~~T~~GTGCG  
CCTTCTCATCAGCTCTCGAGGGT~~G~~ACAGGTGAAAGACCC~~T~~ACAGATCTGACCTCTCC~~T~~GACAGACAACC  
ATCTCTTTTATATTATGCCGCTTCAATCCAACGTTCTCACACTGGAAGAAGAGAGTTCTAATCAGATGCAAC  
GGCCCAAATTCTTGATCTGCAGCTCTGAGTTGGAAAAGAAACCTTCC~~T~~CTGAGTTGCAGAGTT~~C~~AG  
CAATATGATAGGGAACAGGTGCTGATGGGCCAAGAGTGACAAGCATA~~C~~ACA~~A~~CTACTTATTATCTGAGAAGTT  
TTGCTTGTGATCTGAGCCTCTATGAAAGTTAAATATGTAACGCATT~~C~~ATGAATTCCAGTGT~~C~~AGTAAAT  
AGCAGCTATGTGTGCAAAATAAAAGAATGATT~~C~~AGAAAAAA

211/615

FIGURE 210

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59602
<subunit 1 of 1, 223 aa, 1 stop
<MW: 24581, pI: 9.28, NX(S/T): 0
MKFVPCLLLVTLSCLGQAPRQKQGSTGEFHFQTGGGRDSCTMRPSSLGQGAGEVWLR
VDCRNTDQTYWCEYRGQPSMCQAFAAADPKPYWNQALQEILRRLHHACQGAPVLRPSVCREA
GPQAHMQQTSSLKGSPEPNQQPEAGTPSLRPKATVKLTETQLGKDSMEELGKAKPTTR
PTAKPTQPGPRPGGNEAKKKWAHCWKPFQALCAFLISFFRG
```

**Important features:**

**Signal peptide:**

Amino acids: 1-19

**N-myristoylation sites:**

Amino acids: 38-44; 51-57; 194-200

**DNA photolyases class 1 proteins:**

Amino acids: 58-69

**Tyrosine kinase phosphorylation site:**

Amino acids: 64-71

**N-myristoylation sites:**

Amino acids: 38-44; 51-57; 194-200

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids: 4-15

212/615

**FIGURE 211**

GTGCAAGGAGCCGAGGCAGAGATGGCGTCCCTGGCCGGGTCTGCTGGCTGCAGCTCTGCGCACTGACCCAGGCG  
GTCCTCAAACACTGGGTCCCCAACACGGACTTCGACGTGCGAGCCAACGGAGCCAGAACCGGACCCCGTGCGCC  
GGCGCGCCGTTGAGTCCCAGGGACAAGATGGTGTCAAGTCTGGTCAAGAAGGTACGCCGTCTCAGACATG  
CTCCTGCCGCTGGATGGGAACCTCGTCTGGCTTCAGGAGCCGGATTGGCGTCTCAGACGTGGCTCGCACCTG  
GACTGTGGCGCGGGCGAACCTGCCGCTTCAGGAGCCGGACTCTGACCGCTTCTCCTGGCATGACCGCACCTGTGGCGCT  
CTGGGGACGAGGCACCTGGCCTCTTCTCGTGGACGCCGAGCGCGTGCCCTGCCACGACGTCTTCCTTC  
CGCCTAGTGCCTCCTCCCGGTGGGCTCGGCCCTGGCGCTAGCCCGTGCCTGCAGCATCTCGGCTCTGG  
GCCGGACGTTCACGCCGACGAGGACCTGGCTGTTCTGGCGTCCCGCGCGGGCCCTACGCTTCACGGGC  
CGGGCGCGCTGAACGCGTGGGCCCGAGGACTGCGCGAACCGTGGGCTGCGTCTGCGGAAACGCGGAGGCAGC  
CGTGGATCTGCGCGGGCCCTGCTCCAGCCCC

213/615

**FIGURE 212**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59603
<subunit 1 of 1, 197 aa, 1 stop
<MW: 20832, pI: 8.74, NX(S/T): 2
MGVLGRVLLWLQLCAITQAVSKLWVPNTDFDVAANWSQNRTPCAGGAAVEFPADKMVSVLV
QEGHAVSDMLLPIDGEVLVLASGAGFGVSDVGSHLDGAGEPAVFRDSDRFSWHDRTCGAL
GTRHЛАSSSWTPSACPAATTSSFRLVPPSAWGSALALAPCVSAASRLWAGRSRATRTWL
FSWRPARAAYASTGRAR
```

**Important features:**

**Signal peptide:**

Amino acids 1-19

**N-glycosylation site:**

Amino acids 35-39

**Glycosaminoglycan attachment site:**

Amino acids 81-85

**N-myristoylation sites:**

Amino acids 82-88;118-124;153-159

**C-type lectin domain proteins:**

Amino acids 108-118

214/615

FIGURE 213

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTGAGCCTACTCGT  
TTGATTGCAACTATCATGGTGCTGTTGCACTTACCCGTGTTCTGCCCTTTGGTGGCATAACAAGGGA  
CTTGCACCTATCTTCTGCATTTGCAGTCTTGGCATTGACGTGGTACAGCCTTCCTCATACCATTGCAAGG  
GATGCTGTGAAGAAGTGTGTTGCCGTGTGCTTGCATAATTCATGCCAGTTTATGAAGCTTGGAAGGCACTA  
TGGACAGAACGCTGGTGGACAGTTGTAACIATCTCGAAACCTCTGTCTACAGACATGTGCCCTTATCTTGC  
AGCAATGTGTTGCTTGATTGAAACATTGAGGGTTACTTGGAAAGCAACAAACATTCTGAACCTGAATGT  
CAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTGTGGAGTGGAAATCTCCTCATGTACCTGTTCCCTCTG  
ATGTTGTCCCAGTGAATTCCATGAATAACAAACCTATTCAAGAACAGCAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

215/615

**FIGURE 214**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWHNKGALIFCILQSLALTWYSLSFIPFARDAVKKCFAVCLA

216/615

**FIGURE 215**

GGATTTTGTGATCCCGATTGCTCCCACGGGGGGACCTTGTAAGTCGGGGAGGCCAGGACAGGCCACCC  
TGCAGGGGGGGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGCAGAGAGGCCAAGCCCCTTGCTTGGG  
TCACACAGCCAAGGAGGCAGAGGCCAGAACACTACAACCAGATCCAGAGGCCAACAGGGACATGCCACCTGGGACG  
AAAAGGCAGTCACCCCGAGGGCCAAGGGTGGCTCCCGCTGAGAGGATGAGCAAGTCTTAAGGCACCTCACGGTCG  
TGGGAGACGACTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGC  
AGCCACCACCCACACCAGTCTCAGGCAGAGCAGAGCTGCAGCCCCCTGACGTTGCCCCCTGCCCCCTGGCCCCG  
CACCCAGGGCCCCCTTGACATTCAAGGGCATGTTGAGGAAACTGTTGAGCTCCACAGGTTCAAGGTCAAGTCATCATCA  
TCTGCTTGGTGGTCTGGATGCCCTCTGGTCTTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCCGACA  
AGAATAACTATGCTGCCATGGTATTCCACTACATGAGCATCACCATCTGGTCTTTTATGATGGAGATCATCT  
TTAAATTATTGTCTTCCGCCTGAGTTCTTCAACCACAAGTTGAGATCCTGGATGCCGCTGTTGGTGGTCT  
CATTCACTCTGGACATGTCCCTCTGGTCCAGGAGCACCAAGTTGAGGCTCTGGCCTGCTGATTCTGCTCCGGC  
TGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTAGTTAACACAGTTAGAAGACAGCAACTCTAACGGT  
AAAAACAGATGAATGTACAATTGCCGCCAACATTCAACACCTTGAGTTCAAGCTCTGGCTGAGAAGGCCCTGGACT  
GATGAGTTGCTGTATCAACCTGTAAGGAGAAGCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTA  
CTCTCACACAGCCACCGTGAAGACTCTGGAGTAAATGTGCTGTGACAGACTGGCAGTTACATTCACTTCAGATTACA  
ATGTTCACTGGCTGGTGTACGACAGAGAACCTGACAGTCAGTTACATTCACTTCAGATTACA  
CAGAGCATCTGCCCTGTTCAATCACAGAGAACCAAAACAAAAATCTATAAAAGATATTCTGAAAATATGACAGAA  
TTTGACAAATAAAAGCATAAACGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

217/615

FIGURE 216

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEAAAAAQPPTPVSGEEGRAAAPDVA  
PAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVLDALLVLAELILDLKIIQPDKNYAAMVFHYMSITILVFF  
MMEIIFKLFVFRILSSFTTSLRSWMPVVVVSVILDIVLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSE  
RQLLRLKQMNQLAAKIQHLEFSCSEKPLD

218/615

FIGURE 217

GGAAGGCAGCGCAGCTCCACTCAGCCAGTACCGAGATACGCTGGAACCTCCCCAGCCATGGCTTCCCTGGGG  
CAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTGGCTTGCT  
ATTCAGGGAGACACTCCATCACAGTCACTGTGCGCTCAGCTGGAACATGGGGAGGATGGAATCCTGAGC  
TGCACCTTTGAACCTGACATCAAACCTCTGATATCGTACATGGCTGAAGGAAGGTGTTTAGGCTGGTC  
CATGAGTCAAAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTCAGAGGGCGGACAGCAGTGGT  
GATCAAGTGAATGGCAATGCCCTTGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGT  
TATATCATCACTCTAAAGGCAAGGGATGCTAACCTGAGTATAAAACTGGAGCCTTCAGCATGCCGAAGT  
AATGTGGACTATAATGCCAGCTCAGAGACCTTGGCTGTGAGGCTCCCGATGGTCCCCCAGCCCACAGTGGTC  
TGGCATCCAAAGTGGACCAGGGAGCCAACCTCTCGGAAGTCTCAAATACCAGCTTGAGCTGAACCTGAGAAT  
GTGACCATGAAGGTTGTCTGTGCTACAATGTTACGATCAAACACATACTCCTGTATGATTGAAAATGAC  
ATTGCCAAGCAACAGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGAGTCACCTACAGCTGCTAAAC  
TCAAAGGCTCTCTGTGTGCTCTCTTCTTGCCATCAGCTGGCACTTGTGCTCTCAGCCCTAACCTGATG  
CTAAAGAATGTGCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCAC  
CACCAGATATGACCTAGTTTATTTCTGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAG  
AGCAAGAAACAAAAGAAGCAGGAAAGCAGAAGGCTCAAATATGAACAAGATAATCTATCTCAAAGACATATTA  
GAAGTTGGAAAATAATTGTAAGTGTGAACTAGACAAGTGTGTTAAGAGTGATAAGTAAAATGCACGTGGAGACAAGT  
GCATCCCAGATCTCAGGGACCTCCCCCTGGCTGTACCTGGGAGTGAGAGGACAGGATAGTGCATGTTCTTG  
TCTCTGAATTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGGCCCTGGAAAGTCTATCCAAACATATCCA  
CATCTTATATTCCACAAATTAGCTGTAGTATGTACCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAG  
GGCGGCTGCATTTAGTAATGGTCAAATGATTCACTTTATGATGCTTCAAAGGTGCCTTGGCTCTCTTC  
CCAAGTACAACGACAATGCCAAAGTTGAGAAAAATGATCATAATTAGATAAACAGAGCAGTCGGGACACCGATT  
AAAAAAAAA

219/615

**FIGURE 218**

MASLGQIILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEGV  
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF  
SMPEVNVDYNASSETLRCEAPRWFPQPTVWWASQVDQGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSC  
MIENDIAKATGDIKVTESIEIKRRSHLQLLNKASLCVSSFFAISWALLPLSPYLMK

220/615

**FIGURE 219**

GAATTTGAGAAGACAGCGGCCTGCCATGGCGCGTCTCTGGGGCAGGTGTTGGCTCTGGTGTGGTGGCCGCT  
CTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCCTCCGCCGGCCTGCAGCGGGTCATGAGCCGACCTGGGCT  
CAGCAGTTGCTACAGGAGATGAAGACCCCTTCTGAATACTGAGTACCTGATGCCCTTCCTCAACCAGTGT  
GGATCCCTCTCTATTACCTCACCTGGCATCGACAGATCTGACCTGGCTGTGCCATCTGTAACTCTCTGGCT  
ATCATCTTCACACTGATTGTTGGGAAGGCCCTTGGAGAAGAGATATTGGTGGAAAACGTAAGTTAGACTACTGCGAG  
TGCAGGGACGCAGCCTGTTGATCTGCACATACCTGTGTTAGTCCCTCCCAGAACCCATCTCCCCAGAGTGGGCTG  
AGGACACAGGCTTTCCATCCTGCCCTTCCCTGCAGCTGTTGCTCCTGTGGCCATCAGAGTCCCTTC  
CCCTGGACAGTCTGGAGAAAGACAGAGGCTGGGTTGGGATTGAAGACCAGACCCATCTGAGCCCTCCCTCCA  
GCCCTGTACCACTGGCATGGCTGAGCTCAGACCCCTCTGATTCTGCCTATTATCCCAGGAGCAGTTG  
CTGGCATGGTGTCAACCGTGATAGGAATTCACTCTGCATCACAGCTCAGTGAGTAAGACCCAGGGCAACAGT  
CTACCCCTTGAGTGGCCGAACCCACTTCCAGCTCTGCCTCCAGGAAGCCCTGGGCCATGAAGTGTGGCA  
GTGAGCGGATGGACCTAGCACTTCCCTCTGGCCTTAGCTTCCCTCTTATGGGGATAACAGCTACCTCA  
TGGATCACATAAGAGAACAGACTGAAAGAGTTTGTIAACCTTCAAGTGCTGTTAGCTGCGGGGATTAGCAC  
AGGAGACTTACGCTCACCTCAGCAACCTTCTGCCCTCAGCAGCTCTTCCCTGCTAACATCTCAGGCCCTCCAG  
CCCAGCCACCATTACTGTGGCCTGATCTGACTATCATGGTGGAGGTTCCATGGACTGCAGAACTCCAGCTGCA  
TGGAAAGGGCCAGCTGCAGACTTGAGCCAGAAATGCAAACGGGAGGCCTCTGGGACTCAGTCAGAGCGCTTGG  
CTGAATGAGGGGTGGAACCGAGGGAGAGAGGTGCGTCGGAGTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCT  
TGCCTGCCCAACCCATGAGGTAGGCAGAAATCCTCACTGCCAGCCCCCTCTAAACAGGTAGAGAGCTGTGAGGCC  
CAGCCCCACCTGACTCCAGCACACCTGGCGAGTAGCTGTCAATAATCTATGTAAACAGACAAAAAA  
AA

221/615

**FIGURE 220**

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLLQEMKTLFINTEYLMPFLLNQCGSLLYYLTL  
ASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFPILP  
FPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

222/615

FIGURE 221

CTTCTGAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTAGGCTCCAGCTTCTCTGTGGAAGATGACAGCA  
ATTATAGCAGGACCCCTGCCAGGTGTCGAAAAGATTCCGAATAAAACTTGCAGTGGGAAGTACCTAGTGAAA  
CGGCCTAAGATGCCACTTCTCATGTCCCAGGCTTGAGGCCCTGGTCCCCATCCTGGGAGAAGTCAGCTC  
CAGCACCATGAAGGGCATCCTCGTTGCTGGTATCACTGCAGTGCTTGCAGCTGTAGAATCTCTGAGCTGCGT  
GCAGTGTAATTATGGAAAAATCCTGTGTCACAGCATTGCCTCTGAATGTCCTCACATGCCAACACCCAGCTG  
TATCAGCTCCTCAGCCAGCTCCTCTAGAGACACCAGTCAGATTATACCAAGAATATGTTCTGCTCAGCGGAGAA  
CTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGCTGAAGAACACTTCATTTGTAAGCCA  
GTGCTGCAAGGAAAGGAATGCAGCAACACCCAGCGATGCCCTGGACCCCTCCCTGAAGAACGTGTCCAGCAACGC  
AGAGTGCCCTGTTATGAATCTAATGAACTTCCGTGCGTGGGAAGGCCCTGGAAATGCTATGAAGAAGAAC  
GTGTGTCTTCTAGTTGAGAACTTAAGAATGACATTGAGTCTAAAGAGTCTCGTGTGAAAGGCTGTTCCAACGT  
CAGTAACGCCACCTGTCACTTCCGTGAGGAGTCATCTGGAGGACTCTTCAAGCTGGGCTCAAAGCTCCCTCTA  
TGCAAATGTAACAGCTTAACCCCCACGTCACCAACCTTCCACAACGTTGAGGACTCTTCAAGCTGGGCTCAAAGCTCCCTCTA  
CCTCTTGCCCTTGCAGCCTCTTCTGGGACTGCTGCCCTGAGGTCTGAGGTCAGAGCACCCCTGGGTGCTGACACCCCTTTCCCTGCTCTGCCCCGTTAA  
CTGCCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCCTGTTCTTCAATTAAAGCACTGG  
TTCATTCACTGCCAaaaaaaaaaaaaaaaaaaaaaaa

223/615

FIGURE 222

MKGILVAGITAVLVAAVESLSCVQCNWEKSCVNSIASECPSHANTSCISSASSSLETPVRLYQNMFCSAENCS  
EETHITAFTVHVSAAEHFHVSQCCQGKECSNTSDALDPLKNVSSNAECPACYESNGTSCRGKPWKCYEEEQCV  
FLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENKTLGGVIFRKFECANVNSLTPTSAPTTSHNVGSKASLYLL  
ALASLLLRLGLP

224/615

FIGURE 223

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCAGGGCTGCCTCAC  
TGGCCACCCCTCCAACCCCCAAGAGCCCAGCCCCATGGTCCCGCCGCCGGCGCTGCTGTGGGTCTGCTGCTG  
AATCTGGGTCCCCGGCGGGGGGCCAACGGCCTGACCCAGACTCCGACCAGAAATGCAGGGTCAGTTACGC  
TTGGGGGCCCATGACCCGCAGCGACTACCGAGCACCGCCGGACTGGTCTTCCCGGAAGACAAGGATAATCTA  
GAGGACGAGAATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTGGCCGCCACG  
GTGTCCACCGGTTAGCCGTCGTCGCCATTAAACGAGGAGGATGGTCTTCAGAAGAGGGGTTGTGATTAAT  
GCCGGAAAGGATAGCACCAGCAGAGAGCTCCCAGCTGCAGCTCCCAATACAGCGGGAGTCCAGCACGAGGTTT  
ATAGCCAATAGTCAGGAGCCTGAAATCAGGCTGACTTCAAGCCTGCCGCCCTCCCGGAGGTCTACTGAGGAC  
CTGCCAGGCTCGCAGGCCACCCTGAGCCAGTGGTCCACACCTGGGTCTACCCGAGCCGGTGGCGTCACCCTCA  
CCCACAGGCATCTCCTGAGGGATCTGCCGCTGGTGCTGATGCCCTGGGGCCCGTGGCATGCCACTGCAAG  
TCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGGCTGCACGGCCTTCCGGGCCCTCGAGTTGGGGCGCTGAGC  
CAGCTCCGACGGAGCACAGCCTTGCACCCATCAACAATGTCCCTGCAACCAGTCCGGGAAGAGTGCCCCTG  
GACACAAGTCTCTGTACTGACACCAACTGTCCCTCAGAGCACCCAGTACAGGACCACCAACTACCCCCCTTC  
CCCACCATCCACCTCAGAAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTGGAAACGG  
GTCAGGATTGGCCTGGAGGATATTGGAATAGCCTCTTCAGTGTTCACAGAGATGCAACCAATAGACAGAAAC  
CAGAGGTATGGCCACTTCATCCACATGAGGAGATGTCAGTTCTCAACTCTTGCCCTTCAATCCTAGCAC  
CCACTAGATATTTTAGTACAGAAAAACAAATGGAAAACACAA

225/615

**FIGURE 224**

MVPAAGALLWVLLNLGPRRAAGAQGLTQTPTEMQRVSLRGPMTRSYRSTARTGLPRKTRIILEDENDAMADAD  
RLAGPAAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSRELPSPNTAGSSSTRFIANSQEPEIRL  
TSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWPSPTAMPSPEDLRLVLMPWGPWHCHCKSGTMSRSRGK  
LHGLSGRIRVGALSQLRTEHKPCTYQQCPONRLREECPLDTSLCDTNCASQSTTSTRTTTPFPTIHRLSSPSL  
PPASPCPALAFWKVRIGLEDIWNSLSSVTEMQPIDRNQR

226/615

FIGURE 225

CCGGGGTCGACCCACCGTCCGGGGAGAAAGGATGGCCGGCCTGGCGCGGGTTGGTCTGCTAGCTGGGCAG  
CGGCCTGGCGAGCGCTCCCAGGGCACCCTGAGCCGGTGTACCGCAGCTGCGTACTGCAGTGCAGAGAGCAGA  
ACTGCTCTGGGGCGCTCTGAATCACTTCCGCTCCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCTGTC  
GGGACGACTGTAAGTATGAGTGTATGTTGGGTCAACCGTGGCTCTACCTCCAGGAAGGTACAAAAGTGCTCAGT  
TCCATGGCAAGTGGCCCTTCTCCGGTCTCTGTTCTTCAAGAGCCGGCATGGCCGTGGCCTCGTTCTCAATG  
GCCTGGCCAGCCTGGTGTATGCTCTGCCGCTACCGCACCTTGTGCCAGCCTCCCTCCCCATGTACCAACACCTGTG  
TGGCCTTCGCTGGGTGTCCCTCAATGCAATGGTCTGGTCCACAGTCTTCCACACCAGGGACACTGACCTCACAG  
AGAAAATGGACTACTTCTGTGCTCCACTGTCATCTACACTCAATCTACCTGTGCTGCGTCAGGACCGTGGGGC  
TGCAGCACCCAGCTGTGGTCAGTGCCTTCCGGCTCTCTGCTCATGCTGACCGTGCACGTCTCTACCTGA  
GCCTCATCCGCTCGACTATGGCTACAACCTGGTGGCAACGTGGTATTGGGCTGGTCAACGTGGTGGTGGC  
TGGCCTGGTGCCTGTGGAACCCAGCGGGCTGCCCTCAOGTGCAGTGGTGGTGGTGGTCTGCTGCTGCAGG  
GGCTGTCCTGCTCGAGCTGCTTGAACCTCCACCGCTCTCTGGGATGCCATGCCATCTGGCACATCA  
GCACCATCCCTGTCCACGCTCTTTCACTTCTGGAAAGATGACAGCCTGTACCTGTGAAGGAATCAGAGG  
ACAAGTTCAAGCTGGACTTGAAGACCTGGAGCAGACTGCCCCAGTGGGATCTGCCCCCTGCCCCCTGCTGGCCTC  
CCTTCTCCCTCAACCTTGAGATGATTCTCTTTCAACTTCTGAACATGGGACATGAAGGATGTGGGCCAG  
AATCATGTGGCCAGCCCACCCCTGTTGCCCTCACAGCCTGGAGTCTGTTCTAGGGAAAGGCCCTCCAGCATC  
TGGGACTCGAGAGTGGGAGCCCTCACCTCTGGAGCTGAACCTGGGTGGAACTGAGTGTGTTCTAGCTCTA  
CCGGGAGGACAGCTGCTGTTCTCCCCACCAGCCTCTCCCCACATCCCCAGCTGCCCTGGTGGTCTGGAAG  
CCCTCTGTCTACCTGGAGACCAGGGACCACAGGCCCTAGGGATACAGGGGGTCCCTCTGTTACCAACCCCCCA  
CCCTCTCCAGGACACCACCTAGGTGGTGTGGATGCTTGTGTTGGCCAGCCAAGGTTCACGGCGATTCTCCCC  
ATGGGATCTTGAGGGACCAAGCTGCTGGATTGGAAAGGAGTTCACCTGACCGTTGCCCTAGCCAGGTTCCA  
GGAGGCCTCACCATACTCCCTTCAGGGCCAGGGCTCCAGCAAGGCCAGGGCAAGGATCTGTGCTGCTCTGG  
TTGAGAGCCTGCCACCGTGTGTCGGGAGTGTGGCCAGGCTGAGTCATAGGTGACAGGGCCGTGAGCATGGGCC  
TGGGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTTGTCGGGAACAGGTGTGGCTCAAAG  
TGTGTGTGTGCGAGGGGTGGGTGTGTTAGCCTGGGATAGGGAAACGTGTGCGCCTGCTGGTGGCATGTGAGA  
TGAGTGACTGCCGGTGAATGTGTCACAGTTGAGAGGTGGAGCAGGATGAGGAATCCTGTCACCATCAATAAT  
CACTTGTGAGGCCAGCTCTGCCAACGCCACCTGGCGAGGCCAGGAGCTCTCATGGCCAGGCTGCC  
GTGTGCATGTTCCCTGTCTGGTGCCCTTGTGCCCTCTGCAACCTCACAGGGTCCCAACACAGTGGCC  
TCCAGAACGCCCCCTGGAGGGAGAGGAAGGAAATGGGATGGTGGGCTCTCCATCCTCTTCTCT  
TGCCTTCGCATGGCTGCCCTTCCCTCAAAACCTCCATTCCCCGCTGCCAGCCCCCTTGTGCCATAGCTGATTT  
TGGGGAGGAGGAAGGGCGATTGAGGGAGAAGGGGAGAAAGCTTATGGCTGGGTCTGGTTCTCCCTTCCAG  
AGGGTCTTACTGTTCCAGGGTGGCCCAAGGGCAGGCAGGGCCACACTATGCCGTGCCCTGGTAAAGGTGACCC  
CTGCCATTACCAAGCAGCCCTGGCATGTTCTGCCCAAGGAATAGAATGGAGGGAGCTCCAGAAACTTCCAT  
CCAAAGGCAGTCTCGTGGTTGAAGCAGACTGGATTGGCTCTGCCCTGACCCCTTGTCCCTTGTGAGGGA  
GGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTAGCTGGCTAGCTCTTTGATACTGAAAACCTTT  
AAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAATCAATTCCAAGCCTCAAAAAAAAAAAAAAA

227/615

**FIGURE 226**

MAGLAARLVLLAGAAAALASGSQGDREPVYRDCVLQCEEONCSGGALNHFRSRQPIYMSLAGWTCRDDCKYECMWV  
TVGLYLQEKGHKVPQFHGKWPFSRFLFFQEPASAVASFLNGLASLVMLCRYRTFVPPASSPMYHTCVAFAWVSLNAW  
FWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVRTVGLQHPAVVSAFRALLMLTVHVSYLSLIRFDYGYNL  
VANVAIGLVNVVVWWLAWCLWNQRRLPHVRKCVVVVLLLQGLSLLLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFS  
FLEDDSLYLLKESEDKFKLD

**Important features:**

**Signal peptide:**  
amino acids 1-20

**Transmembrane domains:**

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

**N-glycosylation site.**  
amino acids 40-44

**N-myristoylation site.**  
amino acids 43-49

**CUB domain proteins profile.**  
amino acids 285-302

**Amiloride-sensitive sodium channels proteins.**  
amino acids 162-186

228/615

FIGURE 227

TTGGGCTTCCGTAGAGGAAGTGGCGGGACCTTCATTTGGGTTTGGTCCCCCTTCCCCTCCCCGGGGTC  
TGGGGGTGACATTGCACCGCGCCCTCGTGGGTCGCGTTGCCACCCCACGCAGACTCCCCAGCTGGCGGCC  
TCCCATTGCGCTGTCTGGTCAGGCCCCACCCCCCTTCCCACCTGACCAGCATGGGGCTGCGGTTTTGT  
GCTGCACTTTCGTCGCGTTGGCCGGCTCGCGCTTTCTTGATCACTGTGGCTGGGACCCGCTTCCGCTTA  
TCATCCTGGTCGAGGGGCATTTCCTGGCTGGCTCCCTGCTCCCTGGCCTGTGGTCTGGTCACTTGGTCC  
ATGTGACCGACCGGTCAAGATGCCGGCTCCAGTACGGCCTCTGATTTGGTGTGCTGTCTGTCTTCTAC  
AGGAGGTGTTCCGCTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAAGGGTAGCATCGCTGAGTGAGGACG  
GAAGATACCCATCTCCATCGCCAGATGGCTATGTTCTGGTCTCTCCCTCGGTATCATCAGTGGTGTCTTCT  
CTGTTATCAATATTTGGCTGATGCACTTGGCCAGGTGTTGGGATCCATGGAGACTACCCATTACTTCC  
TGACTTCAGCCTTCTGACAGCAGCCATTATCCTGCTCATAACCTTTGGGAGTTGTGTTCTTGATGCCCTGT  
AGAGGAGACGGTACTGGGCTTGGGCTGGTGGTGGAGTCACCTACTGACATCGGGACTGACATTCTGAACC  
CCTGGTATGAGGCCAGCCTGCTGCCATCTATGCACTGTTCATGGGCTCTGGCCTTATCACAGCTG  
GAGGGTCCCTCCGAAGTATTCAAGCAGCCCTTGTAAGGACTTGACTACCTGGACTGATGCCGTGACAGATCC  
CACCTGCCCTGCCACTGCCATGACTGAGCCCAGCCCCAGCCGGTCCATTGCCACATTCTCTGCTCCCT  
CGTCGGCTACCCCACTACCTCCAGGGTTTGCTTGTCTTGTGACCGTTAGTCTCTAAGCTTACAGGAG  
CAGCCTGGGTTCAAGCAGTCAGTACTGGTGGTTGAATCTGCACTTATCCCACCCACCTGGGACCCCTTGT  
TGTGTCCAGGACTCCCCCTGTGTCAGTGTCTGCTCACCCCTGCCAAGACTCACCTCCCTCCCTCTGAGG  
CCGACGGCAGGAGGACAGTCGGGTGATGGTGTATTCTGCCCTGCGCATCCACCCAGGGACTGAGGGACCTAGG  
GGGGACCCCTGGGCTGGGTGCCCTCTGATGTCCTGCCCTGTATTTCTCATCTCAGTTCTGGACAGTGC  
GGTTGCCAAGAAAAGGGACCTAGTTAGCCATTGCCCTGGAGATGAAATTAAATGGAGGCTAAGGATAGATGAGC  
TCTGAGTTCTCAGTACTCCCTCAAGACTGGACATCTGGTCTTTCTCAGGCCCTGAGGGGAACCATTGG  
TGTGATAAAATACCCCTAAACTGCCCTTTTTCTTGTAGGTGGGGAGGGAGGTATATTGGAACTCTTCT  
AACCTCCTGGCTATATTTCTCCTCGAGTTGCTCCCTCATGGCTGGCTCATTCGGTCCCTTCTCCTTGG  
TCCCAGACCTGGGGAAAGGAAGGAAGTCAGTGCATGTTGGAAACTGGCATTACTGGAACTAAATGGTTTAAACCTCC  
TTAACCAACAGCATCCCTCCTCTCCCCAAGGTGAAGTGAGGGTGTGTGGTGAAGCTGGCAACTCCAGAGCTGCA  
GTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGGAGATTTTGTAGTTTAATTGGGG  
TGTGGGAGGGCGGGGAGGTTCTATAAAACTGTATCTGCTGAGGGTGGAGTGTCCCATCCTTTAATC  
AAGGTGATTGTGATTGACTAATAAAAAAGAATTGTAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

229/615

**FIGURE 228**

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLOQYGLLIFG  
AAVSVLLQEVFRRFAYYKLLKADEGLASLSLEDGRSPISIQRQMAVSGLSFGIISGVFSVINILADALGPVVGIH  
GDSPYYFLTSAFLTAIIILLHTFWGVVFFDACEERRRYWALGLVVGSLLTSGLTFLNPWYEASLLPIYAVTVSMG  
LWAFITAGGSLRSIQRSLLCKD

230/615

**FIGURE 229**

CGGGAGGCTGGTCGTCAATGATCCGACCCATTGTCGGCCTCTGCCATGCCCTGCTCTCCCAGGCTCCCGCG  
GCCGACCCCCCGCGAACATGCAAGCCCACGGCCCGCAGGGTTCCCGCGCTCAGCCGGGTATCTGCGGCCTC  
TGCTGCTCCTGCTACTGCTGCTGCTGCCAGCCGTAACCCGCGGGAGACCACGCCGGCGCCCCCAGAG  
CCCTCTCCACGCTGGCCTCCCCAGCCCTTCAACCACGCCGTTGCTCCAGGCCCTCACTACCCAGGCCCTCA  
CTACGCCAGGCACCCCCAAAACCTGGACCTCGGGCTCGCGCAGGCCCTGATGCGGAGTTCCACTCGTGG  
ACGGCCACAATGACCTGCCAGGTCTGAGACAGCGTACAAGAAATGTCAGGATGTTAACCTGCGAAATT  
TCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGTGGGTGCCAGTTCTGGTCAGCCTCCGTCT  
CATGCCAGTCCCAGGACCAGACTGCCGTGCCCTGCCCTGGAGCAGATTGACCTATTCACCGCATGTGTGCC  
CCTACTCTGAACCTGAGCTTGTGACCTCAGCTGAAGGCTGAACAGCTCTCAAAGCTGCCCTGCCATTGGCG  
TGNAGGGTGGTCACTCACTGGACAGCAGCCTCTGTGCTGCCAGTTCTATGTGCTGGGTGCCCTACCTGA  
CACTTACCTTCACCTCGCAGTACACCATGGCAGAGAGTCCACCAAGTTCAAGACACCACATGTACACCAACGTCA  
GCGGATTGACAAGCTTGGTGAGAAAGTAGTAGAGGGAGTTGAACGCCCTGGCATGATGATAGATTGTCCTATG  
CATCGGACACCTTGATAAGAAGGGTCTGGAAAGTGTCTCAGGCTCTGTGATCTCTCCACTCAGCTGCCAGAG  
CTGTGTGTGACAATTGTTGAATGTTCCCGATGATATCTCGCAGCTCTGAAGAACGGTGGCATCGTGTGGTGA  
CACTGTCCATGGGGTGTGCTGCAGTGCACCTGCTGCTAACGTGTCCTGTGGCAGATCACTTGACACACATCA  
GGGCAGTCATTGGATCTGAGTTCATGGGATTGGTGGAAATTATGACGGGACTGGCCGGTCCCTCAGGGGCTGG  
AGGATGTGTCCACATACCCAGTCCTGATAGAGGGAGTTGCTGAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTG  
TCCTTCGTGGAAACCTGCTGCCGGTCTCAGACAAGTGGAAAAGGTGAGAGAGGGAGAGCAGGGCGCAGAGCCCCG  
TGGAGGCTGAGTTCCATATGGCAACTGAGCACATCTGCCACTCCACCTCGCTGCCCTCAGAACATGGACACCAGG  
CTACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCTGGAGGTCTCAAATGCCCTCCCATACCTTG  
TTCCAGGCCTTGTGGCTGCCACCATCCCAACCTTCACCCAGTGGCTCTGCTGACACAGTCGGTCCCCGAGA  
GGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCTAGTTCATTACAAGCATATGCTGAGAATAAACATGTTA  
CACATGGAAAA

231/615

**FIGURE 230**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817  
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown  
><MW: 53569.32, pI: 7.68, NX(S/T): 5  
MOPTGREGSRALSRRYLRRLLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPSALTPGLTPGTP  
KTLDLGRGAQALMRSFPLVDGHNDLPOVLRQRYKNVLQDVNLRFNFSHGOTSLDRLRDGLVGAQFWSASVSCQSQD  
QTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSSQKLAQCLIGVXGGHSLDSSLVLSVRSFYVLGVRYLTFTC  
STPWAESSTKFRHHMYTNVSGLTSFGEKVVEELNRIGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNL  
LNVPDDILQLLKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDVSTY  
PVLIEELLSRXWSEEELQGVLRGNLLRVFRQVEKVRREESRAQSPVAAEFPYGQLSTSCHSHLVPQNGHQATHLEV  
TKOPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC

**Important features of the protein:**

**Signal peptide:**  
amino acids 1-36

**Transmembrane domain:**  
amino acids 313-331

**N-glycosylation sites.**  
amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**  
amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359,  
357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**  
amino acids 136-146

232/615

FIGURE 231

GCTCTGGCGGCCCGCGATTGGTCACCGCCCGTAGGGACAGCCCTGGCTCTGATTGGCAAGCGCTGG  
CCACCTCCCCACACCCCTTGCAGCCTCCCAGTAGGGAGAAAGGAGTAGCTATTAGCCAATTGGCAGGGCCC  
GCTTTTAAAGCTTGATTCCTTGAAGATGAAAGACTAGCGGAAGCTCTGCCTCTTCCCCAGTGGCGAGGG  
AACTCGGGCGATTGGCTGGGAACTGTATCCACCCAAATGTCACCGATTCTCTTCTATGCAGGAAATGAGCAGAC  
CCATCAATAAGAAATTCTCAGCCTGGCGAAAATGGTGGCCCCACGAAGCCACGACAACGGAGGCAAAGAGG  
GTTGCTCAACGCCCCGCTCATTGAAAACCAAATCAGATCTGGACCTATATAGCTGGCGGAGGCGGGCGAT  
GATTGTGCGCTCGCACCCACTGCAGCTGCACAGTCGCATTCTTCCCCGCCCTGAGACCCCTGCAGCACCA  
TCTGTCATGGCGCTGGCTGTTGGTTGAGCGCTGCCGTCTTGGCGCAGCGCAGGGCTCCCG  
GCCGCCCGCGTCCGCTGGAAATCTAGCTTCTCAGGACTGTGGTCGCCCGTCCGCTGTGGCGGGAAAGCGGCC  
CCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCCAGACTCC  
CATGGTTATGACAAGGACCCGTTGGACGTCTGGAACATGCGACTTGTCTTCTTGGCGCTCCATCATC  
CTGGTCTTGGCAGCACCTTGTGCCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGGAAGCTGAG  
AGGCTTGTGAAATACCGAGAGGCCAATGGCCTTCCCACATGGAATCCAACGTGTTGACCCAGCAAGATCCAG  
CTGCCAGAGGATGAGTGACCAGTTGCTAAGTGGGCTCAAGAAGCACCGCCTCCCCACCCCTGCCTGCCATT  
TGACCTCTCAGAGCACCTAATTAAAGGGCTGAAAGTCTGAA

233/615

**FIGURE 232**

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPS A VAGKRPPEPTTPWQEDPEPEDE NLYEKNPDSHG  
YDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAERLVKYREANGLPIMESNCFDPSKIQLPEDE

234/615

FIGURE 233

GGGGCGGCTATGCCGTTGCTCTGCTCGTCTGTGCTCCTGGGGCCCGGGCTGGTCAGAACCCCCA  
CGCGACAGCTCGGGAGGAACCTGTCACTACCCCCGCTGCCTCCGGGACGTAGCCGCACATTCCAGTTCCGC  
ACCGCCTGGGATTGGAGCTTCAGCGGGAAAGGAGTGTCCCATTACAGGCTCTTCCAAAGCCCTGGGGCAGCTG  
ATCTCCAAGTATTCTACGGGAGCTGCACCTGTCAATTACACAAGGCTTTGGAGGACCAGATACTGGGGCCA  
CCCTCCTGCAGGCCCCATCAGGTGCAGAGCTGGGCTGGTCCAAGACACTGTCACTGATGTGGATAAATCT  
TGGAAGGAGCTCAGTAATGTCCCTCAGGGATCTCTGCCTCTCAACTCATCGACTCCACCAACAGTC  
ACTCCCACGTCCCTCAAACCCCTGGGCTGGCAATGACACTGACCACACTTCTGCCTATGCTGTGCTG  
CCGGGGAGGTGGCTGCACCGAAAACCTCACCCCTGGAAGAAGCTTGGCCCTGAGTCCAAGGCAGGCTC  
TCTGTGCTGCTGAAGGCAGATCGCTTGCACACCAGTACCAACTCCCAGGCAGTGCATATCCGCCCTGTTGC  
AGAAATGCACGCTGTACTAGCACTCTCTGGGAGCTGAGGCAGACCCCTGTCACTGTTGATTTGATGCCCTCATCAG  
GGGCAGGGAAAGAAAGACTGGTCCCTCTCCGGATGTTCTCCCGAACCCCTCACGGAGGCCCTGGCTTCA  
GAGAGCCGAGTCTATGGACATCACCAACTACAACCCAGAACAGACATTAGAGGTGACCCACCCCGACC  
ACTACATATCAGGACGTCACTTGGCACTCCGAAAGACATGCCATCTGACTTGCCTGACACCGCCATGATC  
AACAACTCTGAAACCTCAACATCCAGCTCAAGTGGAAAGAGACCCCAAGAGAAATGAGGCCCTCAGTGCCT  
CTGCATGCCAGGGTACGTGAGTGGCTATGGCTGCAAGAGGGGAGCTGAGCACACTGCTGTACAACACCCAC  
CCATACCGGGCTTCCGGTGCTGCTGGACACCGTACCCCTGGTATCTGCGGCTGTATGTGACACCCCTCAC  
ATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCCACTACCAGCCTGCCAGGACCCGCTGCAACCCAC  
CTCCTGGAGATGCTGATTCACTGGCCAACTCAGTCACCAAGGTTCCATCCAGTTGAGCGGGCGCTGCTG  
AAGTGGACCGAGTACAGCCAGATCTAACCATGGCTCTATGTCAGCCCATCTGTCCCTCAGGCCCTGTGCCC  
AGCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGACTCCCTCTCAACAGCTGTTCCAGTCTGTGATGGC  
TCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCCGACACCGGACTTCAGCATGCCCTAC  
AACGTGACTGCCCTACGTGCACGTGGTGGCTGCTACGGCTCCCTCACATCTCCACCCGAACCTTC  
CACATCGAGGAGGCCACAGTGGCTGGCAAGCGGCTGGCCAACCTTATCCGGCGGCCCGAGGTGTCCCC  
CCACTCTGATTCTGCCCTTCCAGCAGCTGCTGGCTTGAACCAAAGTGCCCTGGACCAGGTGAGGCCCTACAGCTGTGTTG  
TGCCACTTGTCTCTCAGAGTTGGCTTTGAACCAAAGTGCCCTGGACCAGGTGAGGCCCTACAGCTGTGTTG  
CCAGTACAGGAGGCCACGAGCAAATGTGGCAATTGAATTGAATTAACTTAGAAATTCAATTCCCTCACGTAGT  
GGCCACCTCTATATTGAGGTGCTAATAAGCAGGAGTGGTGGCTGCTGTTGGACAGCACAGAAAAAGAT  
TTCCATCACCACAGAAAGGTGGCTGGCAGCACTGGCCAAGGTGATGGGTGTGCTACACAGTGTATGCACTGT  
GTAGTGGATGGAGTTACTGTTGTGAATAAAACGGCTTTCCGTGGAAAAAAAAAAAAAA

235/615

**FIGURE 234**

MPLALLVLLLLGPAGWCLAEPGRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHYRLFPKALGQLISK  
YSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDKSWKELSNVLSGIFCASLNFDSTNTVTPT  
ASFKPGLGLANDTDHYFLRYAVLPREVVCCTENLTPWKKLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNA  
RCTSISWELRQTLSVVFDAFITGQGKKDWSLFRMFSRTILTEPCPLASESRVYVDITTYNQNETLEVHPPPTTY  
QDVILGTRKTYAIYDILLTAMINNSRNLNQIQLKWKRPPENEAPPVFLHAQRYYVSGYGLQKGELSTLLYNTHPYR  
AFPVULLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANSVTKVSIQFERALLKWT  
EYTPDPNHGFYVSPSVLSALVPSMVAAKPVDWEESPLFNSLFPPSDGSNYFVRLYTEPLLVLNLPTPDFSMPYNVI  
CLTCTVVAVCYGSFYNLLTRTFHIEEPRGGGLAKRLANLIRRARGVPPL

236/615

FIGURE 235

TGACGTCAAATCACCATGGCCAGCTATCCTTACCGCAGGGCTGCCAGGAGCTGCAGGACAAGCACCAGGAGC  
CCCTCCGGGTAGCTACTACCCCTGGACCCCCAATAGTGGAGGGCAGTATGGTAGTGGCTACCCCTGGTGGTGG  
TTATGGGGTCTGCCCCCTGGAGGGCCTATGGACCACCAGCTGGAGGGCCCTATGGACACCCCCTGGTGGTGG  
GATGTTCCCTCTGAACTCCAGGAGGACCATATGGCGGTGCAGCTCCGGGGCCCTATGGTCAGCCACCTCC  
AAGTTCCCTACGGTGCCTCAGCCTGGCTTATGGACAGGGTGGCCTCCAAATGGTGGATCCTGAGGCCTA  
CTCCTGGTCCAGTCGGTGGACTCAGATCACAGTGGCTATATCTCATGAAGGAGCTAAAGCAGGCCCTGGTCAA  
CTGCAATTGGTCTTCATTCAATGATGAGACTGCCTCATGATGATAAACATGTTGACAAGACCAAGTCAGGCCG  
CATCGATGTCTACGGCTCTCAGCCCTGTGAAATTCCAGCAGTGGAAAGAACCTCTCCAGCAGTATGACCG  
GGACCGCTGGGCTCATTAGCTACACAGAGCTGCAGCAAGCTGTCCCAAATGGGCTACAACCTGAGCCCTTA  
GTTCACCCAGCTCTGGTCTCCGCTACTGCCACGCTGCCAATCCTGCCATGCAGCTGACCGCTTCATCCA  
GGTGTGCACCCAGCTGCAGGTGCTGACAGAGGCTTCCGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCT  
CAGCTTCGAGGACTTCGTACCATGACAGCTCTCGGATGCTTGACCAACCATCTGTGGAGAGTGGAGTGAC  
CAGGGACCTTCTGGCTTCTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTCTGTCCCTCTAGAAGAAC  
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCAAATAGTGAGG  
ACCGGGGCTGAGGCCACAGATAGGGCCTGATGGAGGAGAGGATAGAAGTTGAATGTCTGATGGCATGAGC  
AGTTGAGTGGCACAGCCTGGCACAGGAGCAGGTCTTGAATGGAGTTAGTGTCCAGTCAGCTGAGCTCCACCC  
TGATGCCAGTGGTGAAGTGTTCATCGGCCTGTTACCGTTAGTACCTGTGTTCCCTCACCGGCCATCCTGTCAAAC  
GAGCCCATTCTCAAAGTGGAACTGACCAAGCATGAGAGAGATCTGTCTATGGGACAGTGGCTGGATTCT  
GCCACACCATAATCCTGTGTTAACTCTAGCTGCCCTGGGCTGCCCTGCTCAGACAAATCTGCTCCCTG  
GGCATCTTGGCCAGGCTCTGCCCTGCAAGCTGGGACCCCTCACTTGCCTGCCATGCTCTGCTCGGCTTCAGT  
CTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTAATTGCATTTTTCAATTGGGCCAAAG  
TCCAGTGAATTGTAAGCTCAATAAAAGGATGAAACTCTGA

237/615

**FIGURE 236**

MASYPYRQCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYGHPNPGMFPSG  
TPGGPYGGAAPGGPYGQPPPSSYGAQQPGLYQGGAPPNDPEAYSWFQSVDSDHSGYISMKELKQALVNCNWSS  
FNDETCCLMMINMFDKTKSGRIDVYGFSAWKFIIQQWKNLFQQYDRDRSGSISYTELQQALSQMGYNLSPQFTQLL  
VSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREKDTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-  
83, 83-88, 87-92, 110-115

238/615

**FIGURE 237**

239/615

**FIGURE 238**

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPALDPRSNDLARV  
PLKLSVPPSDGFPPAGGSQVRWPPSWGLPAMDSWPPEDPWQMMAAAEDRLGEALPEELSYLSSAALAPGSGB  
LPGESSPDATGLSPEASLLHQDSESRRLPRNSNLGAGGKILSQRPPWSLIHRVLPDHPWGTLNPSVSWGGGPGBT  
GWGTRPMPHPEGIWINQPPGTSGWNINRYPGGSWGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPNGV  
LRPPGSSWNIIPAGFPNPPSPRIQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263, 259-264, 269-  
274, 270-275, 280-285, 281-286, 305-310

240/615

**FIGURE 239**

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCCTGCTGTGCCCGCGCTGCGCCG  
CTGCTACCGCGTCTGCTGGACGCCGGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCGGAGAGCTCAAGCGCCC  
AGCTCTGCCCGAGGAGCCCAGGCTGCCCGTGACTCCCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCT  
GGGTGGTGTCACTCCCCCTGGGGCTGCTGTTCTGGTCTGCGGATCCAAAGGCTACCTCCTGCCAACGTCACCTCT  
CTTAGAGGAGCTGCTCAGCAAATACCAGCACAAACGAGCTCTCACTCCGGGTCCGAGGCCATCCCCAGGGAGGA  
CAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCGAGCCTCAGGCCTCAACATGGAGTACAT  
GGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGTGGGGCTGGGCCACCAGCCTGCTGTGTTCCCCAG  
CCAGCTGTTCCCCAGCCAGTGCCTGATGGCTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTG  
TTCTGTTTGTTGTTGAGACAGGGTCTCACCTGCCACTGACGCTGGAGTGCAATGGCACAAATCGTCA  
TGCCCTGAAACCTTAGACTCCCGGGTTAAGCGATCCTGCTTCAGGCTCCAAAGTAGCTGAACTACAGGCATGC  
ACCATGGTGCCCAGCTAGATTTAAATATTGTTGGAGATGGGGTCTTGCTACGTTGCCAGGCTGGCTTGAA  
CTCCTAGGCTCAAGCAATCTCCCTGCCTCAGCCTCTCAAAGTGTCTAGGATTATAGGCATGAGTCACCCCTGCTG  
CTCTGGCTCTGTTCTAACATTGCTTAAACACAGCTCTGGGTTCCCTGTGAGAGCTGCTGGCTCGCTCGTGCCT  
ATGTCACTCTGGTAGCTCCACTGGAAACACAGCTCTAGGCTTCCCTGTGAGAGCTGCTGGGAGGGGGCC  
AGGGCTGGCTTGTGATGCTGATCTCAGCTGTGCCACAGCTAGTGCACCCCTGACTTCTCCTAGGCC  
TGTGAGGCTCACTTCCACTTGGAGAGTCCTCCTCGCTGGTTGCCATGACTGTGAGATAAGTCGAGGCTGTGA  
AGGGCCCGGCACAGACTGACCTGCCCTCCCCAACCCCTAGGCTTGCTAACCGGAAAGGAGCTAACGGTGA  
AGACAGCCAAGGTCAACCCCTCCGGGTGATTGATGGGTGTTCCAGGTGTTGGCGATGCTACTTGAC  
CCCAAGCTCCAGTGTGAAACTTCTTCTGGCTGGTTCCAGAACTACAGAGGAATGGACCAACAGTCTTCCAG  
GGTCCCTCTCGTCCACCAACCAGGAGCCTCCACCTGGCCATCCGTCAGCTATGAATGGTTAAACAAACC  
CACGTCCCAGCCTGGTAACATGGTAAAGCCCGTCTCTACAAAAAAATCCAAGTTAGCGGGCATGGTGGTG  
CACCTGTAGTCCCAGCTGCAGTGGACTGAGGTGGAGGTGGGGAGCTGAGGAAGGAGGATCG  
TTGAGCCTGGGAAGTCCGAGGCTGAGCTGAGATTGACCACTGCACCTCCAGCCTGGGTGACAGAGCAAGAC  
CCTGTCCTAAAAAA

241/615

**FIGURE 240**

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLEEELLSKYQHNESHSRVRAIPREDKEEILMLHNKLRGQVQPQAS  
NMEYMVSAAGSGRRGWHRGWGLGHQPALFSQLCSPASACDGWLKVSSGRGGSRLCSVLFVCFTGSHSATDAGVQ  
WHNRHALKP

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 27-31, 41-45

**N-myristoylation site.**

amino acids 126-132, 140-146

**Amidation site.**

amino acids 85-89

242/615

FIGURE 241

AAGGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGGCCAGTGGCCACTATGGGGTCTGGGCTGCC  
CTTGTCTCCTCTTGACCCCTCCTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAG  
GAGTCTTTCTGACAAATTCTCCTATGAGTCCAGCTCCTGGAAATTGCTTAAAAGCTCTGCCTCCTCCAT  
CTCCCTCAGGGACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCA  
TTGAAGCCTGTGTCCTCTGGCCCGGGCTTTGGGCCGGGATGCAGGAGGCAGGCCCGACCCTGTCTTCAG  
CAGGCCAACCTCCTGAGTGGCAATAAAATTGGTATGCTG

243/615

FIGURE 242

MGSGLPLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFELLEKLCLLHLPSGTSVTLHHARSQHHVVCNT

244/615

**FIGURE 243**

GGCAAGTGGAACCACTGGCTTGGGATTTGCTAGATTTAACTCCTGAAAAATATCCCAGAT  
AACTGTCATGAAGCTGGTAACTATCTTCCTGCTGGTGACCACAGCCTTGTAGTTACTCTGCTACTGCCTTCCT  
CATCAACAAAGTGCCCTTCCTGTTGACAAGTTGGCACCTTACCTCTGGACAACATTCTCCCTTATGGATCC  
ATTAAGCTTCTTCTGAAAACTCTGGGCATTCTGTTGAGCACCTGTGGAGGGCTAAGGAAGTGTGAAATGA  
GCTGGGACCAGAGGCTCTGAAGCTGTGAAGAAACTGCTGGAGGCGCTATCACACTGGTGTGACATCAAGATAA  
AGAGCGGAGGTGGATGGGATGGAAGATGATGCTCCTATCCTCCCTGCCTGAAACCTGTTCTACCAATTATAGAT  
CAAATGCCCTAAATGTAGTGACCCGTGAAAAGGACAATAAGCAATGAATACATTA

245/615

**FIGURE 244**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59855
<subunit 1 of 1, 93 aa, 1 stop
<MW: 10161, pI: 7.39, NX(S/T): 0
MKLVTIFLLVTISLCYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGIVS
EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV
```

**Important features:**

**Signal peptide:**

Amino acids 1-18

246/615

**FIGURE 245**

TGCTAGGCTCTGCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGATCCCTATGACT  
GCAATGTGAGGTGTCGGCTTGTCTGGCCAGCAAGCCTGATAAGCATGAAGCTTATCTTGGTGGCTGTGGT  
CGGGTGTGCTGGTCCCCAGCTGAAGCCAACAAGAGTTCTGAAGAGATATCCGGTGCAAATGCATCTGTCCACC  
TTATAGAACATCAGTGGGACATTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGG  
GCCCATGCCAGTGCCTGCCATGACGTGGAGGCCACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAGCAC  
CACCACCATCAAGGTATCATTGTATCTACCTGTCCGTGGTGGGTGCCCTGTGCTCTACATGGCCTCCTGAT  
GCTGGTGGACCTCTGATCCGAAAGCCGGATGCATACACTGAGCAACTGCACAATGAGGAGGAGAATGAGGATGC  
TCGCTCTATGGCAGCAGCTGTCATCCCTGGGGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAGGTGC  
CCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTCTCGATCGGCACAAGATGCTCAGCTAGAT  
GGGCTGGTGTGGTGGGTCAAGGGCCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAGCAGGGGGCTACTT  
CTCCCTTCCCTCGGTCCAGTCTCCCTTTAAAAGCCTGTGGCATTTTCTCTCTCCCTAACTTTAGAAATG  
TTGTACTTGGCTATTGATTAGGGAAGAGGGATGTGGTCTCTGATCTCTGTGTTGTCTTCTGGGTCTTGGGTT  
GAAGGGAGGGGAAGGCAGGCCAGAAGGGATGGAGACATTGGAGGCTCAGGAGTGGATGCGATCTGTCTC  
TCCTGGCTCCACTTTGCCCTCCAGCTGTGGAGGAAAGCATGGCCAGCATTGAGCTTGGGAATGTGTTACCCCTGG  
TTCAGGAACTCAGTGTCTGGAGGAAAGCATGGCCAGCATTGAGCTTGGGAATGTGTTACCCCTGGAGATAAAGCTGG  
ACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGC  
TGGGCCCCCTGAGCCCACTGGGTCTCAGGGTGCAGTGGAGCTGGTGTGCTGTCCCCCTGTGCACTCTCGCA  
CTGGGCATGGAGTGCCATGCATACTCTGCTGCCGGTCCCTCACCTGCACTTGAGGGTCTGGCAGTCCCTC  
CTCTCCCCAGTGTCCACAGTCAGTGAGCCAGCAGGGTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGA  
ACACCACAGCCCCGTACTTGGGTGCCTCTGTCCTGAACCTCGTTGACAGTGCATGGAGAGAAAATTG  
TCCTCTTGTCTTAGAGTGTGTAAATCAAGGAAGCCATATTAAATTGTTTATTCTCTCA

247/615

FIGURE 246

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278  
<subunit 1 of 1, 183 aa, 1 stop  
<MW: 20574, pI: 6.60, NX(S/T): 3  
MKLLSLVAVVGCLLVPPEANKSSEDIRCKCICPPYRNISGHYNNQNVSKDCNCLHVVEPMPVPGHDVEAYCLL  
CECRYEERSTTTIKVIIIVIYLGVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAASLGGPRA  
NTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

**Important features:**

**Signal peptide:**  
amino acids 1-20

**Transmembrane domain:**  
amino acids 90-112

**N-glycosylation sites.**  
amino acids 21-24, 38-41 and 47-50

248/615

**FIGURE 247**

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAAGAAGGAAAAACTTCTGAGTTCAAAACAACAGA  
CTAGTACTCTAAAGAACTCTTAAAACAATTAACTGTTAGGATTGCAGTTATGATTGGATATTATTTAATTCTGT  
TTCTGATGTTGGGGTCTCCACTGTGTTCTGTGCTATTAAATATTACCATTCAGAAGCTCATTCAAGTGTG  
AAAATGAATGCTTAGTGGATCTGTCCTCTACGCATATGTTACAAATTATCTGGAGTTCTTAATCAATGCAGAG  
TTCCCCCTCCCGATTGTTCTAAATAATTGAAAGATGTCTGCTGGAAAAAGGCATGTATTTAAATCTGTAT  
GATTCTCAACCATCTTAGTTGGAAAGGTCTTGAAAGCCAATGAAATACTTTTTTTCTTGCACTAAT  
CAAGTGAGTGTTACCTTTCACTTAGTAGGATGTGTTACGCTAGTAAAATAGAAACCTGTGTTATTCTCAG  
GTATTTAGAAACAAACAGCCATCATTATTTATTTATGTTGTTCTGGCTGTATTCAAAATTATATTTGG  
GCTATCAAATATTACTTCATTCAATATAAAACAATAGTAGAAGTTGTTACTTAGATATGCTTCAGTTGCA  
TTTCTCAGCCTATGTAAGACTACTTGTGTAATAGCCTTGAAATTACAGTACTGTCCTACTATCTTCA  
GATTACTTGATTCAAATAAACCAATTATGTTGTAATTGATATTAATAAAACCAGAATAAAAGTTCATATCTACCC

249/615

FIGURE 248

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFSENECLVDLCLLRICYKLSGVPNQCRVPLPSDCSK

**Important features:****Signal peptide:**

amino acids 1-29

250/615

**FIGURE 249**

AGCGGGTCTCGTTGGGTCGCTAATTCTGTCCGTAGGGCGTGAGACTGAGATTCAAGGGTCTGGGTCCCCGA  
ACCAGGAAGGGTTGGGGAACACAATCTGCAAGCCCCCGCAGCCAAGTGAGGGGCCCGTGTGGGTCTCTCCC  
TCCCTTGCATTCCCACCCCTCGGGCTTGCCTCTGGGACCCCCCTGCCGGGAGATGGCCGCGTTGATG  
CGGAGCAAGGATTGCTCCTGCCTGCTCCTACTGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGAGT  
TCGGGCCAAACTCAACTCCATCAAGTCTCTCTGGCGGGAGACGCCCTGGTCAAGGCCAATCGATCTGCG  
GGCATGTACCAAGGACTGGCATTGGCGGAGTAAGAAGGGCAAAACCTGGGCAGGCCAACCTGTAGCACT  
GATAAGGAGTGTGAAGTGGAGGTATTGCCACAGTCCCCACCAAGGATCATGGCCTGCATGGTGTGCGGAGA  
AAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCAGTACCCGCTGCATAATGGCATCTGTATCCCAGTT  
ACTGAAAGCATCTAACCCCTCACATCCCGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCAATTAC  
TCAAACCATGACTGGGATGGCAGAATCTAGGAAGACCAACACTAAGATGTCACATATAAAGGCATGAAGGA  
GACCCCTGCCATCAGATCATCAGACTGCATTGAAGGGTTTGTGCTGCTGTCATTTCTGGACCAAAATCTGCAA  
CCAGTGTCCATCAGGGGAAGGCTGTGACCAAAACACGCAAGAAGGGTCTCATGGCTGGAAATTTCAGCGT  
TGGCAGTGTGCGAAGGGCCTGCTTGCACAGTATGGAAAGATGCCACACTACTCTCCAAAGCCAGACTCCATGT  
TGTAGAAAATTTGATCACCATGAGGAACATCATCAATTGCGACTGTGAAGTTGTGATTAAATGCAATTAG  
CATGGTGGAAAATAAGGTTAGATGCGAGAAGATGGCTAAATAAGAAACGTGATAAGAATATAGATGATCACAA  
AAAGGGAGAAAGAAAACATGAACACTGAATAGATTAGAATGGGTGACAAATGCGAGTGCAGCCAGTTCCATTATG  
CAACTTGTCTATGTAATAATGTACACATTGTGGAAAATGCTATTATAAGAGAACAGCACACAGTGGAAATT  
ACTGATGAGTAGCATGTGACTTCCAAGAGTTAGGGTGTGCGGAGGAGGGTTCCCTCAGATTGCTGATTG  
TTATACAAATAACCTACATGCCAGATTCTATTCAACGTTAGAGTTAACAAAATACTCCTAGAATAACTGTTA  
TACAATAGGTTCTAAAATAAGGTTGCTAAACAAGAAATGAAACATGGAGCATTGTTAATTACAACAGAAAAT  
TACCTTTGATTGTAACACTACTCTGCTGTTCAATCAAGACTTGTGGTAGATAAGAAAAAAATCAGTCATAT  
TCCAAATAATTGCAAAATAATGCCAGTGTGTTAGGAAGGACAAATAAAACAAACAG  
CCACAAATACTTTTTCAAAATTGTTAGTTACCTGTAATTAAATAAGAAACTGATACAGACAAAACAGTTCC  
TTCAGATTCTACGGAATGACAGTATATCTCTTATCCTATGTGATTCTGCTCTGAATGCAATTATTTCCA  
AACTATACCCATAAAATTGTAACACTGAGTAGTAAATACTTACACAGAGCAGAAATTTCACAGATGGCAAAAAAATTAA  
GATGTCACATATTGTTGAGGAGAGCTAACAGAGAGATCATTATTCTTAAGAGTGGCCATAACCTATATT  
GATAGAAATTGATTGTTAAATACATGTTACATCATACTCTGTTAATAGAGACTTAAGCTGGATCTGACTG  
CACTGGAGTAAGCAAGAAAATTGGAAAACCTTTCTGTTGTCAGGTTGGCAACACATAGATCATGTC  
AGGCACAAGTGGCTGTTCATCTTGAACCAAGGGAGTGCACAGTCAAAATGAATATGCAATTGGGATTGCTAT  
CATATAATTACTATGCAAGATGAATTGAGTGTGAGGTCTGTGTCCTACTATCCTCAATTATTATTATAG  
TGCTGAGATCCTCAAATAATCTCAATTCTAGGAGGTTACAAAATGACTCCTGAGTAGACAGAGTAGTGAGG  
TTTCATTGCCCTCTATAAGCTCTGACTAGCCAATGGCATCATCCAATTCTTCTCCAAACCTGCAAGCATCTG  
CTTTATTGCCAAAGGGCTAGTTCTGTTCTGCAGCCATTGCGTTAAAAAATATAAGTAGGATAACTGTAA  
ACCTGCATATTGCTAATCTATAGACACCAGTTCTAAATTCTTGAACCAACTTACTACTTTTAAACTT  
AACTCAGTTCTAAATACTTTGTCGGAGCACAAACAATAAAGTTATCTTATAGTCGTGACTTTAAACTTTG  
TAGACCACAATTCACTTTAGTTCTTTACTTAAATCCATCTGCAAGTCTCAAATTAAAGTTCTCCAGTAG  
AGATTGAGTTGAGGCTGTTGATATCTATTAAATACTTCAACTTCCACATATAATTACTAAGATGATTAGACTTA  
CATTTCTGCAACAGGCTGCAACAAACAAAATTATAAAACTAGTCCTACAGCAAGAACCAAGTTGTATAAACAGGT  
TGCTATAAGCTGTAAGGAAATGGAACATTCAACATTTCTTATATAACAAATTATTATTTACAATT  
TTGGTTCTGCAATTATTCTTATGTCCACCTTTAAAAAATTATTGAGTAATTATTACAGGAAATG  
TTAATGAGATGTTAGAGATATTCTTACAGAAAGCTTGTAGCAGAAATATTGCAAGCTATTGAC  
TTGTAATTAGGAAATGTTAGGAAATGTTAGGAAATGTTAGGAAATCTTCTCCCTAAACTGAAAAAA  
AAAAAAAAAAAAAAAAAA

251/615

**FIGURE 250**

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLAFGGSKKGKNLGQA  
YPCSSDKECEVGRYCHSPHQGSSACMVCRKKKRCHRDGMCCPSTRCNNGICIPVTESLTPHIPALDGTRHRDR  
NHGHYSNHDLGWQNLRPHTKMSHIKGHEGDPCLRSSDCIEGFCCARHFWTICKPVLHQGEVCTKQRKKGSQGL  
EIFQRCDCAKGLSCKWKDATYSSKARLHVCQKI

**Signal peptide:**  
amino acids 1-25

252/615

FIGURE 251

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAAATCCACCTACCTGGCCTCCCAAAGTGTGGGATTAC  
AGGCCTGAGCCACCGCGCCGCCAACATCACGTTTAAAGGATTGATTCCTCAAATTCAAGCAAATATTCC  
CTTCCCTTAACCTCTTATGTCAGAATGAGGAAGGATAGCTGCATTATTTAGTCAGTTTCAATTGCATAGTAAT  
ATTTTCATGTAGTATTTCTAAGTTATTTAGTAATTCAATATGTTAGATTATAGGTTAACATACTTGTG  
AAAATACTGATGTTTAAAGCCTGGGAGAAATTCTGATTGAGGATTGTTCTTTATCCCCCTTT  
AAAGTCATCCGTCCTTGGCTCAGGATTGGAGAGCTGCACCACAAAAATGGCAAACATCACAGCTCCCAGAT  
TTTGGACCAGTTGAAAGCTCCGAGTTGGGAGCTTACCAACCCCCAAGTACACAGCAGAATAGTACAAGTCA  
CCCTACAACACTACTCTTGGGACCTCAAGCCCCAACATCCCAGCCTCAGTCAGTCACTGACTTCAA  
ATCTCAACCTGAGCCATCCCCAGTTCTTAGCCAGTTGAGCCAGCAGCACACAGCACCAGAGCAGGCAGTCAGTCACTGT  
TCCTCCTCCTGGTTGGAGTCCTTCCCTCCAGGCAAACCTTCGAGAATCAACACCTGGAGACAGTCCCTCAC  
TGTGAACAAGCTTGCAGCTTCCAGCACGACCATTGAAAATATCTCTGTGTCGAGCAGGCCACAGCCCCAA  
ACACATCAAACCTGCTAAGCGGGGATACCCAGCTTCAAGATCCCAGCTCTGCACTGGAAATGCCCAGTT  
AGCAGATGTCACAGGTTAAAGTGCAGTTGGGCTCTGGAATTGGGCTCAGAACCTCTCTGAAATTGG  
ATCAGCTCCAAGCAGTGAACATAGTAATCAGATTCCCACAGCTTGTATTGAAAGTCCTTAAGTGAGCCTTGAA  
TACATCTTATCAATGACCAGTGCAGTACAGAACCTCACATATAACACTTCGTCATTACCTCCTGCAGTCAG  
AAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTCTTATGACCAGAGTTCTGTGCATAACAGGAT  
CCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCAGGAACCATCATGAATGGACATGGTGGTGGTCGAAG  
TCAGCAGACACTAGACAGTAAGTATAGCAGCAAGCTACTCTTGTATGGCTGGTGCACCCAAACAGAGGAAGAG  
GATAGCTCACGTGATGGAAAACACCAGTTGGTCATGGCTATTGTTAAAAAGCAGCCTTTGCTTTTG  
TTTTGGACCAGGTGTGGCTGTGGTTATTAGAAATGCTTAACACAGCAAGAAGGAGGTGGTGGTCTCAT  
TTCTCTGCCATACTGACACTGCACCACAGTCAGCATACAGTATGCATTAAAGATGCTTGGCCAGGCGGG  
GTGGCTGATGCCATACTCCAGTGCTTGGGGCCAAGGCAGGCAAGATTGCCAAGCTCAGGAGTTGAGACC  
ACCCCTGGGCAACATGGTGAACACTCTGTCTACTAAAATACGAAAAGTACAGCCGGTGTGGTGGCGCGCTGCC  
TGTAATCCCAGCTACTTGGGAGGCTGAGGCACAAGAACATCGCTTGAGGCCAGTGGCTACAAAGTGA  
ACTCCGTCAG

253/615

**FIGURE 252**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGEIAPPKMANITSSQILDQLKAPSLGQFTTTPSTQQNSTSHPTT  
TTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPPPGLESFPSQAKLRESTPGDSPSTVNK  
LLQLPSTTIENISVSVHQPQPKHIKLAKRIPPASKIPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAP  
SSENSNQIPISLYSKSLSEPLNTSLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPYQ  
SPVSSSESAPGTIMNGHGGGRSQTLDSKYSSKLLLWLVPTKQRKRIAHVMWKTIVGQWLIR

**Signal peptide:**  
amino acids 1-24

254/615

**FIGURE 253**

GGGCGCCCGCGTACTCACTAGCTGAGGTGGCAGTGGTCCACCAACATGGAGCTCTCGCAGATGTCGGAGCTCAT  
GGGGCTGTCGGTGTGCTTGGGCTGCTGGCCCTGATGGCAGCGCGCGGTAGCGCGGGGGTGGCTGCGCGCGGG  
GGAGGAGAGGAGCGGGCGGCCGCTGCAAAAGCAAATGGATTCCACCTGACAAATCTCGGGATCCAAGAA  
GCAGAAAACAATATCAGCGGATTCGAAGGAGAACGCTCAACAACACAACCTCACCCACCGCTCCTGGCTGCAGC  
TCTGAAGAGGCCACAGCGGGAACATATCTTGACATGGACTTAGCAGCAATGGCAAATACCTGGCTACCTGTGCAGA  
TGATCGCACCACCGCATCTGGAGCACCAAGGACTTCCTGAGCGAGAGCACCGCAGCATGAGAGCCAACGTGGA  
GCTGGACCACGCCACCCCTGGTGCCTGCAGCCCTGACTGCAGAGCCTCATCGTCTGGCTGGCAACGGGGACAC  
CCTCCGTGCTTCAAGATGACCAAGCGGGAGGATGGGGCTACACCTCACAGCCACCCAGAGGACTTCCCTAA  
AAAGCACAAGGCGCTGTCACTGACATTGGCATTGCTAACACAGGGAAAGTTATCATGACTGCCTCCAGTGACAC  
CACTGCTCATCTGGAGGCTGAAGGGTCAAGTGTGCTTACCATCAACACCAACAGATGAACAACACACACGC  
TGCTGTATCTCCCTGTCAGATTGTAGCCTGCTGCTTACCCCAGATGTGAAGGGTTGGGAAGGTCTGCTT  
TGGAAAGAAGGGGGAGTTCCAGGAGGTGGTGCAGGCTTCGAACTAAAGGGCACTCCGGGCTGTGCACTCGTT  
TGCTTTCTCAACGACTCACGGAGGATGGCTCTGTCAGGATGGTACATGGAAAGGACTGTGGGACACAGATGT  
GGAATAACAAGAAGCAGGACCCCTACTTGCTGAAGACAGGCCCTTGAAGAGGGCGGGGTGCCGCGCGTG  
CCGCCTGGCCCTCTCCCCAACGCCAGGCTTGGCCTTGGCAGTGGCAGTAGTATTCACTCTACAATACCCG  
GCGGGCGAGAAGGAGGAGTGCTTGAGCGGGTCCATGGCAGTGATGCCAACATTGTCCTTGACATCACTGG  
CCGCTTCTGGCCTCTGTGGGACCGGGCGGTGCCGTGTTCACAAACACTCTGGCCACCGAGCCATGGTGG  
GGAGATGCAGGGCACCTGAAGCGGGCTCCAACGAGAGCACCGCCAGGGCTGCAGCAGCAGCTGACCCAGGC  
CCAAGAGACCCCTGAAGAGCCTGGTGCCCTGAAGAAGTGAACCTGCTGGGAGGGCCGGCAGAGGATTGAGGAGGA  
GGGATCTGCCCTCTCATGGCACTGCTGCCATTTCTCCCAGGTGGAAGCCTTCAAGAAGGAGTCTCTGGT  
TTCTTACTGGTGGCCCTGCTTCTCCCATTGAAACTACTCTGTCACTTAGGTCTCTCTTGCTGGCTGT  
GACTCCTCCCTGACTAGTGGCAAGGTGCTTTCTCCAGGCCAGTGGTGGAAATCTGTCCTCACCTGGC  
ACTGAGGAGAATGGTAGAGAGGGAGGAGAGAGAGAGAATGTGATTGGCAGCAGCACATCCTCAC  
ACCCAAAGAAGTTGTAATGTTCCAGAACACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTGCAAGGATG  
GGAGACTGGGATAGCTCCCATCACAGAACTGTGTTCCATCAAAAGACACTAAGGGATTCTGGCCTCA  
GTTCTATTGTAAGATGGAGATAATCCTCTGTGAACCTCTTGCAAGAGATGATATGAGGCTAAGAGAATATCA  
AGTCCCCAGGTCTGGAGAAAAGTAGAAAAGAGTAGTACTATTGTCCAATGTGATGAAAGGGTAAAGGGAA  
CCAGTGTGCTTGAAACCAAATTAGAACACATTCCCTGGAGGCAAAGTTCTGGGACTTGATCATACATT  
TATATGGTGGGACTTCTCTCTGGGAGATGATATCTGTTAAGGAGACCTTTCAAGTCAAGTT  
CAGATATTGAGTGCCCACTCTGTGCCAAATAAATATGAGCTGGGATTAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAA

255/615

FIGURE 254

MELSQMSELMGLSVLGLLALMATAAVARGWLRA GEERSGRPACQKANGFPPDKSSGSKKQYQRIRKEKPQQH  
NFTHRLLAAALKSHSGNISCMDFSSNGKYLATCADDRITIRIWSTKDFIQLREHRSRANVELDHATLVRSPDCRA  
FIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKKHKAPVIDIGIANTGKFIMTASSDTTVLIWSILKGQVLSTI  
NTNQMNNTHAAVSPCGRFVASCGFTP DVKWEVCFGKKG EFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKD  
GTWKWLWDTDVEYKKKQDPYLLKTGRFEAAAGAACRLALSPNAQVLALASGSSIHLYNTRGEKEECFERVHGEC  
IANLSFDITGRFLASCGDRAVLFHNTPGH RAMVEEMQGHLKRASNESTRQRLQQQLTQAQETLKSLGALKK

**Important features:**

**Signal peptide:**  
amino acids 1-25

**N-glycosylation site.**

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

**Beta-transducin family Trp-Asp repeat protein.**

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

256/615

**FIGURE 255**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCGGGCCAGGTGCC  
GTCGCAGGTGCCCTGGCCGGAGATGCGGTAGGGAGCGCGAGAAGCCTTCTCGCGCTGCCCTGCTGGCCGCTGG  
GCCACCCAGCCC**ATGG**CGAACCCGGGCTGGGCTGCTTCTGGCGCTGGGCTGCCCTGCTGGCCGCTGG  
GGCGAGGCTGGGGCAAATACAGACCACTCTGCAAATGAGAATAGCACTGTTTGCCCTCATCCACCAGCTCC  
AGCTCCGATGGCAACCTCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTCTCCCTCTGGCTGCCCTGCTC  
CTGGCTGTGGGCTGGCACTGTTGGTGCAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACGGCCCAAGT  
AGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCGGCCCTCAGGACTCCAAGGAGACGGTGCAGGGCTGCC  
CCCATCT**AGGT**CCCCCTCCTGCATCTGCTCCCTCATTGCTGTGACCTGGGAAAGGCAGTGCCCTCT  
GGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGAAAGGTACTCAAAAGACTCTGCCCTGAGGTCAAGAGA  
GGATGGGCTATTCACTTTATATATATAAATTAGTAGTGAAGATGTAAAAAAAAAAAAAAA

257/615

**FIGURE 256**

MANPGLGILLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSDGNLRPEAITAIIVVFSLLAALLLAVG  
LALLVRKLREKRQTEGYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

258/615

**FIGURE 257**

GCAGGAAATAACTAGAGAGGAACAATGGGGTATTAGAGGTTTGTCTTAGTTCTGTGCCTGCTGCAC  
CACTCAAATACTTCCTTCATTAAGCTGAATAATAATGGCCTTGAAGATATTGTCAATTGTTATAGATCCTAGTGTG  
CCAGAAGATGAAAAAATAATTGAAACAAATAGAGGATATGGTACTACAGCTTCTACGTACCTGTTGAAGCCACA  
GAAAAAAAGATTTTTTCAAAAATGTATCTATATAATTCTGAGAATTGGAAAGGAAATCCTCAGTACAAAAGG  
CCAAAACATGAAAACCATAAACATGCTGATGTTATAGTGTGACCAACCTACACTCCCAGGTAGAGATGAACCATAC  
ACCAAGCAGTTCACAGAATGTGGAGAGAAAGGCAGAACATCACTCACCCCTGACCTTCACTTGGAACAAAAAA  
CAAATGAAATATGGGACCAACAGGCAAACIGTTGTCATGAGTGGGCTCACCTCCGGTGGGAGTGTGATGAG  
TACAATGAGATCAGCCTTCTACCGTCTAAGTCAGGAAACAAAGGTGTTCCGCAGGTATCTCT  
GGTAGAAATAGAGTTATAAGTGTCAAGGAGGAGCAGCTGTCTAGTAGAGCATGCAGAATTGATTCTACAAACAAA  
CTGTATGGAAAAGATGTCAATTCTTCTGTATAAGTACAAACAGAAAAGCATCCATAATGTTATGCAAAGT  
ATTGATTCTGTTGTAACGAAAAACCCATAATCAAGAGCTTCAAGCTACAAAACATAAAGTGC  
AATTAGAAGTACATGGGAGGTGATTAGCAATTCTGAGGATTTTAAACACCATACCCATGGTGACACCACCT  
CCTCCACCTGTCTTCATTGCTGAAGATCAGTCAGGAAATTGTGCTTAGTTCTGATAAGTCTGGAAAGCATG  
GGGGGTAAGGACGCCCTAACATGAACTCAAGCAGCAAACATTCTCCTGCAAGACTGTTGAAAATGGATCC  
TGGGGGGATGGTCACTGTGATAGTACTGCCACTATTGTAATAAGCTAACAAATAAAAGCAGTGTGAA  
AGAAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAACTTCCATCTGCTCTGGAATTAAATATGCA  
TTTCAGGTGATTGGAGAGCTACATTCCAACTCAGTGGATCCGAAGTACTGCTGCTGACTGATGGGAGGATAAC  
ACTGCAAGTTCTGATTGATGAACTGAAACAAAGTGGGCCATTGTCATTATTGTTGCTTGGGAGGACTGCT  
GATGAGCAGTAATAGAGTGGCAAGATAACAGGAGGAAGTCATTATTGTTICAGATGAAGCTCAGAACAAAT  
GGCCTCATTGATGCTTTGGGCTCTACATCAGGAAATACTGATCTCTCCAGAAGTCCCTCAGCTCGAAAGT  
AAGGGATTAACACTGAATAGTAAGCTGGATGAAACGACACTGTCTAACATTGATAGTACAGTGGGAAAGGACACG  
TTCTCTCATCACATGGAACAGTCTGGGAGGACTTCCAGTATTCTCTGGGAGTCCAGTGGAAACAATAATGAAAAT  
TTTCAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCCAGGAACCTGCAAAAGGTGGCACTTGGCCTAC  
AATCTTCAAGCCAAAGCGAACCCAGAAACATAACTATTACAGTAACCTCTCGAGCAGCAAATTCTCTGCT  
CCAATCACAGTGAATGCTAAATGAAATAGGACGTAACAGTCTCCAGCCAAATGATTGTTACGCAGAAATT  
CTACAAGGATATCTACCTGTTCTGGGAGGCAATGTGACTGCTTCTGATGAAATCAGAACATGACATACAGAACG  
TTGGAACCTTGGATAATGGTGCAGGCGCTGATCTTCAAGAATGATGGAGTACTCTCAGGTTATTTACAGCA  
TATACAGAAAATGGCAGATATAGCTAAAAGTCGGGCTCATGGAGGAGCAAACACTGCCAGGCTAAATTACGG  
CCTCCACTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGAAATTGAAGCAAACCCGCCAACAGACCT  
GAAAATTGATGAGGATACTCAGACCCATTGGAGGATTTCAGCCGAACAGCATCCGGAGGTGCATTGTGTATCA  
CAAGTCCCAAGCCTCCCTGCCATGGTACCAATACCCACCAAGTCAAATCACAGACCTGATGCCACAGTTCATGAG  
GATAAGGATATTCTTACATGGACAGCAGGAGATAATTGATGTTGAAAAGTTCAACGTTATATCATAAGA  
ATAAGTGCAGTATTCTGATCTAAGAGACAGTTGATGATGCTCTCAAGTAATAACTACTGATCTGTCACCA  
AAGGAGGCAACTCCAAGGAAAGCTTGCAATTAAACAGAAAATATCTCAGAAGAAAATGCAACCCACATATT  
ATTGCCATTAAAGTATAGATAAAAGCAATTGACATCAAAGTATCCAACATTGCAAGTAACCTTGTATC  
CCTCAAGCAAATCCTGATGACATTCTACACCTACTCCTACTCCTACTCCTGATAAAAGTCATAAT  
TCTGGAGTTAATATTCTACGCTGGTATTGTCGTGATTGGGCTGTTGTAATTGTTAACTTTATTAAAGTACC  
ACCATTGAACTTAAAGAAGAAAAATCTCAAGTAGACCTAGAACAGAGGTTTAAACAAACAAATGTA  
GTAAAGGATATTCTGAAATCTTAAATGATCTCCATGTGTGATCATAAAACTCATAAAAATAATTAAAGATGTCG  
GAAAAGGATACTTGTGATTAAATGAAACAAACTCATGGGATATGTAACAGGTTAAATTTAAAGTATTCA  
TTTATTGTTATTGTAAGAAATAGTGTGAAACAAAGATCCTTTTCTACTGATACCTGGTTGTATATT  
ATTGATGCAACAGTTCTGAAATGATATTCAAATTGATCAAGAAATTAAACATCTATCTGAGTAGTCAA  
AATACAAGTAAAGGAGGAGCAAATAACAAACATTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA  
AAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

259/615

**FIGURE 258**

MGLFRGFVFLVLCLLHQSNNTSFIKLNNNGFEDIVIVIDPSVPEDEKILIEQIEDMVTTASTYLFEATEKRFFFKN  
VSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEYIHFTPDLGGKKQNEYGPPG  
KLFVHEWAHLRWGVFDEYNEDQPFYRAKSKEATRCAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQF  
FPDKVQTEKASIMFMQSIDSVVEFCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLL  
KISQRIVCLVLDKGSGMGGKDRLNRMNQAAKFLLQTENGWSWGMVFDSTATIVNKLIQIKSSDERNTLMAGL  
PTYPLGGTSICSGIKYAFQVIGELHSQDGSEVLLLTGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMS  
KITGGSHFYVSDEAQNNGLIDAFLGALTSGNTDLSQKSLQLESKGLTNSNAWMNDTVIIDSTVGKDTFFLITWNS  
LPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKM  
NKDVNSFSPSPMIVYAEILQGYVPVLGANVIAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGRYS  
LKVRRAHGGANTARLKLRRPLNRAAYIPGWVVNGEIEANPRPEIDEDTQTTLEDFSRTASGGAFVVSQVPSLPLP  
DQYPPSQITDLDATVHEDKIIILTWTAPGDNFVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKES  
FAFKPENISEENATHIFIAKSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPDKSHNSGVNISTL  
VLSVIGSVVIVNFILETTI

**Signal peptide:**  
amino acids 1-21

**Putative transmembrane domains:**  
amino acids 284-300, 617-633

**Leucine zipper pattern.**  
amino acids 469-491, 476-498

**N-glycosylation site.**  
amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592, 628-632,  
811-815, 832-836, 837-841, 852-856, 896-900

260/615

**FIGURE 259**

CGCCGGAGGCAGCGGCGGTGGCGACGGCGACATGGCGTTGTCAGAGGACGACTTCAGCACAGTTCAA  
ACTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGCAGTGCTTGAGAAGCTGCTGGACCGCC  
CGCCCCCTGGCTGCAGAGGCCAGGACCGCTCTGTTGACATACATCATCTTCAAGCCTGGCATTGGCA  
GTCTACTGCCATGGAACTTCTTATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCAG  
CCACCGGGAGGACCTGAGGGCTCAGACATCCTGAACACTTTGAGAGCTACCTGCCGTTGCCCTCACCGTGC  
CCTCCATGCTGTGCCTGGCAACTCTGCTGTCAACAGGGTTGCACTGCCACATCCGTGCTCTGGCCTCAC  
TGACGGTCACTCTGGCCATCTCATGGTATACTGCACTGGTAAGGGTGGACACTTCCCTGGACCCGTGGTT  
TTTTGCGGGTCAACCATTGCTGTCACTGGTGCAGCGGTGCCTTCACTGTCTCAGCAGCAGCATCACGGCA  
TGACCGGGCTCCTTCTATGAGGAACCTCCAAGCAGTGAATATCAGGAGGAGCATGGGCGGACGGTCAGCGCCG  
TGGCCTCATGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGCCCTCTCTGACGCCACCA  
TCTTCCTCGTCTGCTGCATGGACTCTACCTGCTGCTGCCAGGCTGGAGTATGCCAGGTACTACATGAGGCCCTG  
TTCTTGCGGCCATGTGTTTCTGGTGAAGAGGAGCTTCCCAGGACTCCCTCAGTGCCTCGGTGGCTCCA  
GATTCAATTGATTCCCCACACACCCCTCTCCGCCCCATCTGAAGAAAGACGCCAGCCTGGGTTCTGTCACCT  
ACGTCTTCTTCATCACCGCCTCATCTACCCCGCGTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCT  
CACTGTGGACCACCAAGTTTCATCCCCCTCACTACCTTCTCTGTACAACACTTGTGACCTATGTGGCTCGGGC  
AGCTCACCGCCTGGATCCAGGTGCCAGGGCCAACAGCAAGGGCGTCCCAGGGTCTGTGCTCCCTGGACCTGCC  
TCATCCCCCTTCTGTGCTGTAACTACCAGCCCCGCGTCCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGT  
ACCCCGCACTCCTCAGCTCCCTGCTGGGCTCAGCAACGGCTACCTCAGCACCTGCCCTCCTCACGGGCTA  
AGATTGTGCCAGGGAGCTGGCTGAGGCCACGGGAGTGGTGAATGTCCTTTATGTGTGCTGGCTTAACACTGG  
GCTCAGCCTGCTCACCTCCTGGTCACCTCATCTAGAAGGGAGGACACAAGGACATTGGTCTCAGAGCCTT  
TGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAGGGCTAAAGTTCACTTGGGACAGAGAG  
CAGAGCACACTCGGGCTCATCCCCCAAGATGCCAGTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATA  
TTCCAGTCATATTAACAGAACACTCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGTACTCCCTCACA  
GCTGATGGTTAACATCCACCTTCTTAGGCCCTCAAAGATGCTGCCAGTGTGCTGCCCTAGAGTTATTACAAA  
GCCAGTGCCAAAACCCAGCCATGGCTCTTGCACCTCCAGCTGCGCTCATCCAGCTGACAGCGAGATGCAA  
GCAAATGCTCAGCTCCCTTACCCGAAGGGTCTCCCTGGAATGAACTCCCTGGCATGGTCAGTCCCTCAGGC  
CCAAGACTCAAGTGTGCACAGACCCCTGTGTTCTGCGGGTGAACAACGTGCCACTAACAGACTGGAAACCCAG  
AAAGATGGCTTCCATGAATGCTTCAATTCCAGAGGGACCAAGAGGGCTCCGTGCAAGGGATCAAGCATGTCT  
GGCCTGGGTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGTCAAGATGAGGGTCTTCA  
GTGTTCTGTTACACATGTCAAAGCCATTGGTCAAGGGCGTAATAAAACTTGGTATTCAAAAA

261/615

**FIGURE 260**

MAVVSEDDFQHSSNSTYGTTS defense domain sequence:  
SSLRADQEALLEKLLDRPPGLQRPEDRFGTYIIFPSLGI  
GIGSLLPWNFFITAK  
EYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFLLVNRAVHIRV  
LASLTVILAIFMVIT  
ALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSIYGMTGSFPMRNSQALISGGAMGGTV  
SAVASLVDLAASSD  
VRNSALAFFLTATIFLVLCMGLYLLLSRLEYARYYMRPVLA  
AHVFSGEEEELPQDSLSAPSVASRFIDSHTPPLRP  
ILKKTASLGFCVTYVFFITSLIYPAVCTNIESLNKGSGSLWTTKF  
IPLTFLLYNFADLCGRQLTAWIQVPGPN  
SKALPGFVLLRTCLIPLFVLCNYQPRVHLKT  
VVVFQSDVYPALLSSLLGLSNGYLSTLALLYGP  
KIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252, 305-330,  
448-472

262/615

**FIGURE 261**

CGGACGCGTGGCTGCTGGGGAAAGGCCAAAGAACCTGGAAAGGCCACTCTCTGGACCACACCTGTTA  
AAGAACCTAACCAATTAAAGCCACTGGAAATTGTCTAGGGTGTGGTGAATAAGGAGGCAGAAT  
GGATGATTCATCTCATTAGCCTGCTGCTGGCATGTTGGGTGATGTTACGTGGCCGAATCATTCCCTT  
GGCTGTTAATTCTCAGAGGAAGCAGTGAAGGACTGAGGAGTACATGCCCTTATGAAGATATTCTGAGGGAAA  
ACACCACCAAGCAACTGA  
GGCAGTCATCGCCTGAAGGAGTACATGCCCTTATGAAGATATTCTGAGGGAAA  
ACACCACCAAGCAACTGA  
AACACATAATGTGATTGATCAGACAAAGCAGCAGAAAAATCAGTGTCCATGAACATGAGCACAGCCACGACCA  
CACACAGCTGCATGCCATATTGGTGTTCCTCGTCTGGGCTCGTTTATGTTGCTGGTGGACAGATTGG  
TAACCTCCATGTGCATTCTACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCAAATCACCACCGCTGG  
TCTGGTTGTCCATGCTGCAGCTGATGGTGTCTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTT  
AATTGTGTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTGGACTGGTTCTTCTTGATGCTGATGCTGG  
CTTAGAGCGGAATCGAATCAGAAAGCATTGCTGGTCTTGCAATTGGCAGCACCAGTTATGTCATGGTGCACATA  
CTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTCAGAGGTGAACGCCACGGGAGTGGCATGCTTTCTCTGC  
CGGGACATTCTTATGTTGCCCCAGTACATGTCCTCCCTGAGGTGGCGGAATAGGCACAGCCACAAGCCCGA  
TGCCACGGGAGGGAGAGGCCTAGCCGCTGGAAGTGGCAGCCCTGGTCTGGTTGCCTCATCCCTCATCCT  
GTCAGTAGGACACCAGCATTAAATGTTCAAGGCTTCCAGCCCTGGTCCAGGGCGTTGCCCATTCCAGTGAGAACAGC  
CGGCACGTGACAGCTACTCCTCAGTCAGTCCTGCGCATCTACATGTATTCTAGAGTCCA  
GAGGGGAGGTGAGGTTAAACAGTGAATGAAAAGCTTGTAGAGTAGAAACACATTACGTTGCAAGTTAGCTA  
TAGACATCCCATTGTTATCTTTAAAGGCCCTGACATTGCGTTTAAATATTCTCTTAACCCATTCTC  
AGGGAAAGATGGAATTAGTTAAGGAAAAGAGGAGAACCTCATACTCACAATGAAATAGTGAATTGAAAATAC  
AGTGTCTGTAATTAAGCTATGTCCTTCTTAGTTAGGGCTCTGCTACTTTATCCATTGATTTTAACAA  
TGGTTCCCACCATGTAAGACTGGTGTCTAGCATCTATGCCACATGCGTGTGGAGGTCAAGCACCACACTCA  
CTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGCAAGACACATTGAAAGCTC  
TCCTTATACTCAAAGAGATATCATTGAAAGGATGCTAGAGGGATTAAACAGCTCCTTGGCACGTGCCT  
CTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGGTGGGAGGAGCTCTAAAGAGGTGACTGGTATT  
TTGAGCATTCCTGTCAAGTCTCCTTGCGAGAATACCTGTCCTCACATTCTAGAGGGAGGCCAGTCTAGT  
AGTTTCAGTCTAGGCTTCTTCAGAAGAACAGTCAGATCACAAAGTGTCTGGAAATTAAAGGATATTAAATT  
TAAGTGAATTGGATGGTATTGATATTCTCTAGCAGATCAGCAATCCCTCTAGGGACCTAAATAGTATGGTGTCC  
TTTTTTTTGTTTTTTTTTAATTATTCTCTAGCAGATCAGCAATCCCTCTAGGGACCTAAATAGT  
TCAGCTTGGCGACACTGTCCTCACAATACCACCTGAGCAAGATGGATCATAATGAGAAGTGTGTTGCCT  
ATTGATTAAAGCTTATTGGAATCATGTCCTGCTCTGCTGGTGTAAATTGTTGTTGAGGATGAATTCTTACAGGACAA  
CCACTCTCGAAGTGAATAATGAAGATAATAATATCTTATTCTTATCCCCCTCAAAGAAATTACCTTGTG  
TCAAATGCCGCTTGTGAGCCCTAAACACCTCCATGTGAAATTGACACAATCACTAATCTGGTAAT  
TTAAACAATTGAGATAGCAGAACAGACTAGGATAATTCTTCTTCAATTGCAAAATTGGTAA  
ACCCCTGCTTGTCAAATAAGTGTATAATTGTTATTATTAAATTCTTACTTCTATACCATTCAAAACACA  
TTACACTAAGGGGAACCAAGACTAGTTCTCAGGGCAGTGGACGTAGTAGTTGTAAGGTTCTATGAC  
GCATAAGCTAGCATGCCATTGATTATTCTCTCATGAAATTGTCAGGGACTGGGATCAGCAGCTGGAAATAAGCTT  
GTGAGCCCTCTGCTGGCCACAGTGAGGAAGTAGCAGCAAAATAGGATACAGTTGTTAGTGTAGTCATTGGCAACAATT  
GCATACAATTCTACTACCAAGAGAAGGTATAAGTATGAAAGTCCAAATGACTCCTGATTGGATGTTAACAGCT  
GACTGGTGTGAGACTTGAGGTTCATCTAGTCCTTCAAACATATGGTGCCTAGATTCTCTGGAAACTGAC  
TTTGTCAAATAATAGCAGATTGAGTGTGTCAAAAAAA

263/615

**FIGURE 262**

MDDFISISSLALMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHALYEDILEGKHHQAS  
ETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVLDQIGNSHVHSTDPEARSSNSKTTTL  
GLVVHAAADGVALGAAASTSQTSQLIVFVAIMLHKAPAAGFLVSFLMHAGLERNRIRKHLIVFALAAPVMSMVT  
YLGLSKSSKEALSEVNATGVAMLFSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLI  
LSVGHQH

**Signal peptide:**  
amino acids 1-18

**Transmembrane domain:**  
amino acids 37-56, 106-122, 211-230, 240-260, 288-304

264/615

**FIGURE 263**

CTCCTTAGGTGAAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACTGTCCCCGG  
GCAGGGGTGACAACAGGTGTCATCTTTGATCTCGTGTGCTGCCTCTATTCAAGGAAGAC  
GCCAAGGTAATTGACCCAGGGAGCAATGATGTAGGCCACCTCCTAACCTTCCCTCTTGAAACCCCC  
AGTTATGCGGAGGTTACTAGAGAGTGTCAACTCACCAGCAGCGCTCCTCGGCTTAACTGTG  
TTGGAGGAGAGAACCTTGTGGGGCTCGTTCTTAGCAGTGTCTAGAAGGTACTGTGCTGAGGGGTG  
GACCAGAAGAAAGGAAAGGTCCCCCTCTTGTGTTGGCTGCACATCAGGAAGGCTGTGATGGGAATGAA  
GGTAAAACCTGGAGATTTCACTTCACTGCTATTGCTCTGCCTGCAAGATCATCCTTAAAGTAGAGA  
AGCTGCTCTGTGTGGTTAACTCCAAGAGGAGCAACTCGTCTAGAAGGAAATGGATGCAAGCAG  
TCCGGGGGCCCCAACGATGCTTCTGTGGCTAGCCCAGGGAAAGGCCCTCCGTGGGGCCCCGGCT  
TTGAGGAGATGCCACCGGTTCTGGACGATGGCTATTCTGATATGATGATGTTCTGGCGGGGTG  
TGCCTGGATTCCCGGGTGGTTTGCTGGTGCCTCTCTGCTGTGCTATCTCTGCTCTGTACATGT  
TGGCTGCACCCAAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGCCAACAGCCCCACGGGAAG  
GAGGGTACCGAGGCCCTCAGGAGTGGGAGGAGCAGCACCGCAACTACGTGAGCAGCGTGAAGCG  
GCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGGAGGTGAGCAGCTCAGGAATGGCGATACCAAG  
CCAGCGATGCTGCTGGCTGGGCTGGACAGGAGCCCCCAGGGAAACCCAGGCCACCTCTGGCC  
TTCTGCACTCGCAGGTGGACAAGGAGGTAATGCTGGGCTCAAGCTGGCACAGAGTATGCAAGC  
AGTGCCTTCGATAGCTTACTCTACAGAAGGTGACAGCTGGAGACTGGCCTAACCGCCACCCCCG  
AGGAGAACGCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGAAGGCCATGAAATGCACTGGGAGAC  
CTGAAACATCTGCAAGGAAACAGGCCCATCACCCTCCTAACCGCCCTGTGATTTCATAGAAGGGAC  
CTACCGAACAGAACAGGGACAAAGGGACATTGTGATGCTCACCTTCAAAAGGGGACCAACACGAAT  
TCAACAGGCTCATCTTATTGACCATTCAGCCCCATCATGAAAAGTGAAGACTCAACATG  
GCCAACAGCTTATCAATGTTATCGTCCTCTAGCAAAAGGGTGGACAAGTCTCGGCAGTTCATGCA  
GAATTTCAGGGAGATGTGCAATTGAGCAGGATGGGAGACTCCATCTACTGTTTACTTGGGAAAG  
AAGAAATAATGAAGTCAAAGGAATACTTGAAGACTTCAAAAGCTGCCAACCTCAGGAACTTAC  
TTCATCAGCTGAATGGGAATTTCCTGGGGAAAGGGACTTGTGATGTTGGAGGCCGCTCTGGAAAGGG  
AAGCAACGTCCTCTCTTGTGATGTTGGACATCTACATCTGAAATTCTCAATACGTGTA  
GGCTGAATACACAGCCAGGGAAAGAAGGTATTTTATCCAGTTCTTCAGTCAGTACAATCTGGCATA  
ATATACGGCCACCATGATGCACTCCCTCCCTGGAACAGCAGCTGGTCAATAAGAAGGAAACTGGATT  
TTGGAGAGACTTTGGATTGGGATGACCTGTCAGTATCGGTCAAGCTCATCAATATAGTGGGTTG  
ATCTGGACATCAAGGCTGGGGCGAGAGGATGTGCACTTTATGCAAGTATCTCACAGCAACTC  
ATAGTGGTACGGACGCTGTGCGAGGACTCTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAGCT  
GACCCCCGAGCAGTACAAGATGTGCACTGCAAGGCCATGAACGAGGCACTCCACGGCCAGCTGG  
GCATGCTGGTGTCAAGGAGAGATAGAGGCTCACCTCGCAACAGAACAGAACAGAACAGTGA  
AAAACATGAACTCCCGAGAACAGGATTGGGAGAGACTTTCTTCTTGTCAATTACTGAAGGTG  
GCTGCAACAGAACAGAACACTTCCATAAACAGGACGACAAAAGAAATTGGACTGATGGTCAAGAGATG  
AGCCTCCGATTCTCTGTTGGCTTTTACAACAGAAATCAAATCTCGTTGCCTGAAAAGT  
AACCCAGTTGCAACCTGTGAAGTGTCTGACAAAGGAGCAATGCTGTGAGATTATAAGCTAATGGTG  
TGGAGGTTTGATGGTGTAAATACACTGAGACCTGTTGCTCATGAAATATTCTATG  
ATTAAAGAGCAGTTGTGAAAAAAATTCTAGGATGAAAGGCAAGCATATTCTCATATGAATGA  
GCCTATCAGGGGCTCTAGTTCTAGGAAATGCTAAATATCAGAACAGGAGAGGAGATAGGCTT  
TTATGATACTAGTGTGATCATTAAGTAAAATGGACCAAGAAAAGAAAAGACATAAAATATCG  
TGTCAATTCTCCCAAGATTAACAAAAATAATCTGCTTATCTTTGGTGTCTTAAACTGTCT  
CCGTTTTCTCTTAAATGCACTTTTCTCCCTGTGAGTTAGTGTGCTTATTTAAATT  
CCACTTGTCAAGCCTTACAAGAGGACACAAGTGGCCTACATTTTATTTAAAGAAGATACTT  
GAGATGCTTATGAGAACATTCTAGTCAAGACATCAAAATGATGCCATATCCAAGGACATGCCAATG  
CTGATTCTGTCAGGCACTGAATGTCAGGCATTGAGACATAGGGAAGGAATGGTTGACTAATACAGA  
CGTACAGATACTTCTCTGAAGAGTATTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATG  
ACACTTCTGTTACAGAAAAGGAAACTCATTCAAGACTGGTGTATCTGATGTACCTAAAAGTCAG  
AAACACATTTCTCCTCAGAACAGTGGGACCTTCTTACCTGTTAAATAACCAAAAGTATACCCT  
GTGAACCAAAACATCTTTCAAAACAGGGTGTCTCTTGCTTCTGCCAGTCAAGAAGGAAATG  
GAGAAAATATATATATATATATATGTAAGGATCAATCATCTGCAAGGAGGAAATCTAGTGGATG  
GAAGTTTGCTACATGTTATCCACCCAGGCCAGGTGGAAAGTAAGTGAATTATTTTAAATTAAAGC  
AGTTCTACTCAATACCAAGATGCTTCTGAAAATTGCAATTATTACCATTTCAAACATTTTTAA  
AATAAAATACAGTTAACATAGAGTGGTTCTCTGTTCACTGTAAGGAAATATTAGCCAGCACAGATG  
GAGCTTAATCTCTTGTGCTTCTGTTGCTTCACTGCAAGCTAAACTCATGTTTAAAGCTTCA  
GAACATTCAAGCTGTGGTGTAAAAATGCAATTGTTATTGATTTGACTGGTAGTTATGAAATT  
AATTAAAACACAGGCCATGAATGGAAGGGTATGCAAGCTAATAAAATATGATTGTGGATATGAA

265/615

FIGURE 264

MMMVRRGILLAWISRVVVLLVILCCAlSVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWEEQHRYVSSL  
KRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLIAFLHSQVDKAEVNAGVKLATEYAAVPFDS  
FTLQKVYQLETGLTRPEEKPVRKDKRDELVEAIESALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYE  
LTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMANTLINVIVPLAKRVDKFRQFMQNREMCEQDGDRVHLTVVY  
FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLLNT  
QPGKKVFPVLFQSQYNPGIIYGHDAVPPLEQQLVIKKETGFWRDEFGFGMTQCYRSDFINIGGFDLGIKGWGGED  
VHLYRKYLHSNLIVVRTPVRLFHLWHEKRCMDELTPEQYKMCMQSKAMNEASHGQLGMLVFRHEIAHLRKQKQ  
KTSSKKT

266/615

FIGURE 265

**GGATGCAGAAAGCCTCAGTGTGCTCTTCCTGGCTGGGCTGCTTACGCTGGCATTGCCCTTTCA**  
**CCAGTGGCTTCCTGCTCACCGTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCCAGGCCCTGGTCCC**  
**TGCCATGGGGAGCCAAGGAAACCTGGGCTGCTGGATGGCTTCCCGATTTCGCGGGTTGTGTTGGTCTGA**  
**TAGATGCTCTCGGATTTGACTTCGCCCCAGCCCCAGCATTACACGGCTCAGAGAGGCCCTCTGCTCCTACCCCT**  
**TCCTGGGAAACTAACGCTCCTTGAGGATCCTGGAGATTAGCAGCCCCCATGCCGGCTCTACCGATCTCAGG**  
**TTGACCCCTCCTACCACCATGCAGCGCTCAAGGCCCTCAGGACTGGCTACTGCCAACCTTATTGATGCTG**  
**GTAGTAACCTCGCAGCCACGCATAGTGGAAAGACAATCTCAATTAGCAGCTCACCAAGTGCAGGAAGGCGTAG**  
**TCTTCATGGGAGATGATACTGGAAAGACCTTTCCCTGGTCTTCTCCAAAGCTTCTTCATCCATCCTCA**  
**ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGAAACACCTTACCCCCACCATGGACAGTGGTGAATGGG**  
**ACGTGCTATTGCTACTTCCTGGTGTGGACACTGTGGCCACAAGCATGGCCCTCACCAACCCGTAATGGCCA**  
**AGAAAATAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGCTGGAGAATGACACACTGCTGGTAGTGG**  
**CTGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGACAGTGAAGCTGGAGGTCTCAGCTGCTCTTTTC**  
**TGTATAGCCCCACAGCAGTCCTCCCAGCACCCCACAGAGGGAGCAGAGGTGATTCTCTCAAGTTAGCCTGTG**  
**CCACGCTGGCCCTGCTGCTGGGCTGCCATCCCATTGGGAATATCGGGGAAGTGAATGGCTGAGCTATTCTCAG**  
**GGGTGAGGACTCCAGGCCACTCCTCTGCTTAGGCTCAGGCTCAGCTCTCATCTCAATGCTCAGCAGGTTG**  
**CCCAGTTCTCATACACTCAGCTGACTACTCAGGACCTTCAGGACTAAGGAGCTTCATCAGCTGAGAACCTCT**  
**TCTCCAGGCCCTGCTGACTACAGTGGCTTCTCAGAGCCCCAAGGGGCTAGGCGACACTGCCGACTGTGA**  
**TTGCTGAGCTGCAGTTCCTGCGGGGAGCTGGGCATGTGCATCGAGTCTGGCTCGTTCTCTGGTCC**  
**GCATGGGGGGGTTACTGCTCTTGGCTGCTTCTGCTTATCTGCTGCTGGCATCTCACTGGCAATATCCC**  
**CAGGCTTCCATTCTGCCCTACTCCTGACACCTGTGGCTGGGCTGGTGGGCAATAGCTATGCTGGAC**  
**TCCTGGGAACTATTGAGCTGAAGCTAGATCTAGTGTCTTAGGGCTGTGGCTGAGCTCATTCTCCCTT**  
**TTCTGTGAAAGCCTGGCTGGCTGGGCTTCAAGAGGCCCTGGCAACCCCTGTTCCATCCCTGGGCCGTCC**  
**TGTTACTCTGCTGTTGCTGGCTGTGTTCTCTGATAGTTGTTGAGCTGAGGCACGGGCCACCCCT**  
**TCCCTTTGGGCTCATTCACTCTGCTCTGGTGTCCAGCTTCACTGGGAGGGCAGCTGCTTCCACCTAACGCTAC**  
**TCACAATGCCCGCCCTGGCATTCAAGCCACAACACCCACGGCACAAATGGTGCATATGCCCTGAGGCTTG**  
**GAATTGGGTTGCTTTATGTAACAGGCTAGCTGGGCTTTCATCGCTGGCCTGAAGAGACACCTGTTGCCACT**  
**CCTCTCCCTGGCTGAGCTCTGGCATCATGGTGGTGGTCAGGCCAAGAATTATGGTATGGAGCTTGTG**  
**CGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTCGCCGCTATGGTATCTCAAGAGCCCCGAGCCAC**  
**CCATGCTTTGTGCCCTGGGACTGCCCTAATGGCATGGTACTGCTGCCACTGGCATTGGCCTGGGCTGAGGG**  
**CAGATGAGGCTCCCCCGTCTGGGCTCTGGCTCTGGGCATCCATGGCTGCCCTGGGCTGAGGG**  
**TGGCTCAGGGCTCGCGCTGCTGCTGGAAAGCCTGTGACAGTGTGGTAAGGCTGGGCCAGGCCCTCAA**  
**GGACCAGGACTGTCCTCACTCCCTCTCAGGCCCTGGGACTTCTCAAGCTGACTGGATTATGTGGCCCTCAA**  
**TCTACCGACACATGCAGGAGGAGTCCGGGCCGTTAGAGAGGACCAATCTCAGGGTCCCTGACTGTGGCTG**  
**CTTATCAGTTGGGAGTGTCTACTCAGCTGCTATGGTACAGGCCCTCACCCCTGTTGGCTTCCACTCTGCTGT**  
**TGCATGCCGAGCGCATCAGCTGTTCTGCTGCTGCTGGCTTCTGCTGCTGCTGCTGCTGCTGCTG**  
**CTGGGATAACCGCTCACAGGCCACCAGCCGCTTCTGGCATCCATTGGCATGCGCTTCTGGGCCCTCATGGCCA**  
**CACAGACCTCTACTCCACAGGCCACCAGCCGCTTCTGGCATGCGCTTCTGGCATGCGCTTCTGGGATTCC**  
**CAGAGGTGATGGCTCTGACTTGGCTGCCCTTGTAGTGGGAGGCCAACACCTTGCTCTCCACCTCTCT**  
**TTGCAGTAGGTTGCCACTGCTCTGCTGGCTTCTGCTGAGAGTCAGGGCTGCCAGAGAGACAGCAGC**  
**CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGGAGGAAGAGGAGGCCACTGATGGAGATGCCCTGGG**  
**ATGCCCTCAGCACTCTATGCACTGCTGCACTGGCTCAAGTACCTCTTATCTGGTATTCACTGATTC**  
**TGGCCTGTGCCCTGGCAGCCCTCATCTGCCAGGCATCTCATGGTCTGGAAAGTGTGCTTGGCCCTAAGTCATAT**  
**TGAGGCTGTGGCTCATTGTGAGCAGCGTGGGACTTCTCTGGCATAGCTTGGTGTAGAGAGTGGATGGTG**  
**CTGTGAGCTCTGGTCTGGCAGCTATTCTGGCCAGAGGAGCTAGCCTAGTGTGATTACTGGCACTGGCT**  
**ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCTGACAGGACTGGATGATCTGCAAGACAGGCTCAGCCATAC**  
**TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATCTATAATTCAAGGACACAGTGGAGTA**  
**TGATCCCTAACCTCTGATTGGATGCACTGAGGGACAAGGGGGCGCTCCGAAGTGGAAATAAAATAGGCCG**  
**GGCTGGTGAATTGCCACCTATAATCCCAGCATTGGGAGGCAGAGTGGAGGATTGCTTGGCTCCAGGAGTTCA**  
**AGACCAGCCTGTGGAACATAACAAGACCCGCTCTACTATTAAAAAAAGTGTAAATAAAATGATAATAT**

267/615

**FIGURE 266**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTLELTNHSSCQEPPPGPGSLPWGSQGKPGACWMASRFSRVVLVLI
DALRFDFAQHQSHVPREPPVSLPFLGKLSSIQRILEIQPHHARILYRSQVDPTTMQRLKALTTSGLPTFIDAG
SNFASHAIVEDNLIKQLTSAGRVVFMGDDTWKDLFPGAFSKAFFPSFNVRDLDVDNGILEHLYPTMDSGEWD
VLIAHFLGVDHCGHKHGPHHEMAKKLSQMDQVIQGLVERLENDTLIVVAGDHGMTNGDHGGDSELEVSAALFL
YSPTAVFPSTPPEEPEVIPQVSLVPTLALLLGLPIPFGNIGEVMAELFSGGEDSQPHSSALAQAQASALHINAQQVS
RFLHTYSAATQDLQAKEHLQQLNLF SKASADYQWLLQSPKGAEATLPTVIAELQQFLRGARACMIESWARFSLVR
MAGGTALLAASCFCICLLASQWAISPGFPFCPLLLTPVAWGLVGAIAYAGLLGTIELKLDLVILGAVA AVSSFLPF
LWKAWAGWGSKRPLATLFPPIP GPVLLLLFRЛАVFFSDSFVVAEARATPFLLGFSFILLLVQQLHWEGQLLPPKLL
TMPRLGTSATTNPPRHNGAYALRIGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGRAKNLWYGACVA
ALVALLAAVRLWLRRYGNLKSPEPPMMLFVRWGLPIMALGTAAYWALASGADEAPPRLRVLVSGASMVLPRAVAGL
AASGLALLWKPVTIVKAGAGAPRTTRTVLTPSGPPTSQADLDYVVPQIYRHMQEEFRGRLERTKSQQGPLTVAA
YQLGSVYSAAMVTALTLLHAERISLVSFLLLFLQSFLLLHLLAAGI PVTTPGPFTV PWQAVSAWALMAT
QTFYSTGHQPVFPVPAIHWHAAFGVGFPEGHGSCTWLPA LLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKRQQP
PGNEADARVRPEEEEPPLMEMRLRDAPQHFYAALLQLGLKYL FILGIQILACALAASILRRHLMVWKVFAPKFIF
EAVGFIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034,  
1052-1070**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271

268/615

FIGURE 267

GAGACTGCAGAGGGAGATAAGAGAGAGGGCAAAGAGGGCAGCAAGAGAGTTGTCCTGGGGATCCAGAAACCCATG  
ATACCCCTACTGAACACCGAATCCCCTGGAAGGCCACAGAGACAGAGACAGCAAGAGAGATAAACACT  
CACGCCAGGAGCTCGCTCGTCTCTCTCTCTCTACTCCTCCCTCCCTCTCTGCTGCTAGTCCT  
CTAGTCCTCAAATTCCCAGTCCCCCTGCACCCCTCTGGGACACTATGTTCTCCGCCCCCTGCTGGAGGTG  
ATTTGGATCCTGGCTCGAGATGGGGTCAACACTGGACGCTATGAGGGCCACATGGTCAGGACCATTGGCCAGCC  
TCTTACCTCTGAGTGGAAACAATGCCAGTCGCCATCGATATTGAGACAGACAGTGTGACATTGACCTGAT  
TTGCTGCTCTGCAGCCCCACGGATATGACCAGCCCTGGCAGGCTTGGACCTGCACAAACAATGGCACACA  
GTGCAACTCTCTGCCCTCACCTGTATCTGGGTGGACTTCCCCAAAATATGAGCTGCCAGCTCACCTG  
CACTGGGTCAGAAAGGATCCCCAGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTGAGAGCTCCAC  
ATTGTAACATTGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGGCCTAGGGCCTGGCTGCTG  
GGCATCTTAATTGAGGTGGGTGAGACTAAGAATATAGCTATGAACACATTCTGAGTCAGTGCATGAAGTCAGG  
CTAAAGAGTCAGAAGACCTCAGTGCCTCCCTCAACCTAAAGAGAGCTGCTCCCCAACAGCTGGGCAGTACTTC  
CGCTACAAATGGCTCGCTACAACCCCCCTGCTACCAGAGTGTGCTGGACACTTTTATAGAAGGTCCCAG  
ATTTCAATGAAACAGCTGGAAAAGCTTCAGGGACATTGTTCTCCACAGAAGAGGGAGCCCTTAAGCTTGGTA  
CAGAACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGCTTGTCTCTGCCTTCTCCTGGCTGTTATTTC  
ACACAGGTGAAATGCTGAGTCTAGGTGAGGAATCTGGGTGGCTGTCTCTGCCTTCTCCTGGCTGTTATTTC  
ATTGCTAGAAAGATTGCGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCAGCACAGCCACGACT  
GAGGCATAAATTCCCTCTCAGATACCATGGATGTGGATGACTTCCCTCATGCCTATCAGGAAGCCTCTAAATG  
GGGTGTAGGATCTGGCAGAAACACTGTAGGAGTAGTAAGCAGATGCTCTCTTCCCTGGACATCTTAGAGA  
GGAATGGACCCAGGCTGTCAATTCCAGGAAGAAGTGCAGAGCCTCAGCCTCTCAAACATGTAGGAGGAATGAG  
GAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTAGTTGCAAGGGAAAGTTGGGATATAACCCCAAAGTC  
CTCTACCCCTCACTTTATGGCCCTTCCCTAGATATACTGCAGGGATCTCCTTAGGATAAAAGAGTTGCTGTT  
GAAGTTGTTATTTGATCAATATAATTGGAAATTAAAGTTCTGACTTT

269/615

FIGURE 268

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPLPALQPHGYDQPGTE
PLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDSDSYDSLSEA
AERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPCYQSV
LWTVFYRRSQISMEQLEKLOGTLFSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTGEMLSLGVGILVG
CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

270/615

**FIGURE 269**

GTGGCGCTGGCGGTTGCTGTCAGCTGATTCCCGGGTTGGTGGCAGCGGGCGTAGCAGCAATGGACTTTCTCCTGG  
GGGAACCCGTTCAGCTCTCCAGTGGACAGCGCATCGAGAAAGCCACAGATGGCTCCCTGCAGAGCGAGGACTGG  
GCCCTCAACATGGAGATCTGCGACATCATCAACAGAGACGGAGGAAGGTCCCAAAGATGCCCTCCGAGCAGTAAAG  
AAGAGAACATGTTGGGAATAAGAACTTCCACGGAGGTGATGCTGGCTCTCACAGTCTTAGAAAACCTGTGTCAGAAC  
TGCAGGGCACCCTTCCACGTGCTGGTGGCCAGGACTTCGTGGAGAGTGTGCTGGTGAGGACCATCCTGCC  
AAGAACAAACCCACCCACCATCGTGCATGACAAAGTGCTAACCTCATCCAGTCTGGCTGACGCGTCCGCAGC  
TCGCCCCGATCTGACAGGTGTGGTCACCATCTATGAGGACCTGCGGGAGGAAGGGCTGGAGTCCCCATGACTGAC  
CTGGACATGCTGTACCCATCCACACACCCAGAGGACCGTGTCAACTCAGAGACACAATCAGGACAGGATTCTG  
TGGGCACTGACTCCAGCCAGCAAGAGGACTCTGGCCAGCATGCTGCCCTCTGCCCGCCCCGCCATACTCTCG  
GTGACACGCCCATAGCACCAACCCCGAACAGATTGGGAAGCTGCCAGTGAGCTGGAGATGGTGAGTGGGAACG  
TGAGGGTGATGTCGGAGATGCTGACGGAGCTGGTGCCACCCAGGGCGAGCCCGCAGACCTGGAGCTGCTGCAGG  
AGCTCAACCGCACGTGCCAGGCCATGCAGCAGCGGGTCTGAGTGATACCCCTGCTCCGGGCCATGCCCAAGGA  
GCCCTTCAGAGCCCCACACTGCCAGTCGAGGGCTGGCTGGAGGCTGGCCACAGTGGAAATTCTGCCGAGCCTATTG  
TCCCCTACCCCTGCTCTGCTGCATGGGGCCCCATGGCTTGGCTGCCACTGAGGGTAGGGTAGGGTGAGGAGG  
CCCCCTGAGGAGCTGCCAGGCCAGGTACGAAGCTGCAACTCTGCCAGTGGCGAGATCTCATCAGCCCCA  
GGCTGCAGGTGAGGCTTCAGGGGATGCTGGGGCCCCACTGCCCTCCGCTGCCCTCCATCCTTCTCTGT  
TCCCTCTGGCCGGGACCCACAGCACTGGGCTCACCTTGGTGTACTGGAGAGGTGCCCTTTG  
TATCCCCAATTAAAGGTAGAAAAC

271/615

FIGURE 270

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62813
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23465, pI: 7.57, NX(S/T): 1
MDFLLGNPFSSPVGQRIEKATD GSLQSEDWALNMEICDIINETEEGP K DALRAVKKRIVGNKNFHEVMILALT VLE
TCVKNCGHRFHVLVASQDFVESVLVRTILPKNNPPTIVHDKVNLIQSWADAFRSSPD LTGVVTIYEDILRRKGLE
FPMTDLDMLSPIHTPRGPCSTQRHNQDRILWALTPASKRTL ASMLPLCPPRPYSPVTRP
```

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-15

**N-glycosylation site:**

Amino acids 41-45

**N-myristoylation sites:**

Amino acids 6-12; 23-29

272/615

FIGURE 271

CGGACGCCGTGGCGGACCGTGGCGGACCGTGGGTCTCTGCAGGAGACGCCAGCCTGCCTGCCATGGGGC  
TCGGGTTGAGGGGCTGGGACGTCCTCTGACTGTGCCACCGCCCTGATGCTGCCGTGAAGCCCCCGCAG  
GCTCCTGGGGGGCCAGATCATCGGGGCCACGAGGTGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCT  
TCGGGGGCCAACATCACTGCGGAGGCTTCCTGCTGCGAGCCCCTGGGTGGTCTCGGCCGCCACTGCTTCAGCC  
ACAGAGACCTCCGCACTGGCCTGGTGGTGCTGGGCCACGTCCTGAGTAACGCGGAGGCCACCCAGCAGGTGT  
TTGGCATCGATGCTCTCACACGCACCCGACTACCAACCCATGACCCACGCCAACGACATCTGCCTGCTGCC  
TGAACGGCTCTGCTGTCCTGGCCCTGCAGTGGGCTGCTGAGGCTGCCAGGGAGAAGGGCAGGCCACAG  
CGGGGACACGGTGCCGGTGGCTGGCTGGGCTTCGTGACTTTGAGGAGCTGCCCTGGACTGATGGAGG  
CCAAGGTCCGAGTGCTGGACCCGACGTCGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCA  
CCCGCAGTGGGGACAGCCACAGACGGGGCTCTGCTCGGCCGACTCGGAGGGCCCTGGTGTGCAGGAACCGGG  
CTCACGGCCTCGTTCTCTCGGGCCTCTGGTGGGCGACCCCAAGACCCCGACGTGTAACCGCAGGTGTCCG  
CCTTGTCGGCTGGATCTGGGACGTGGTGGCGGACCGACTCCCCAGCCGGCCCCCTGCCCTGGGACCACCAAGC  
CCCCAGGAGAAGGCCCTGAGCACAACCTGCGGATGCAAATGAGATGGCCCTCCAGGGCTTGGAAATGTTCCG  
TGGCTGGGCCCCACGGGAAGCCTGATGTTCAAGGGTTGGGACGGGAGCGGTGGGACACCCATTCCACA  
TGCAAAGGGAGAAGCAAACCCAGTAAATGTTAACTGACAAAAAAAAAAAAAAAAGAAA

273/615

**FIGURE 272**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pi: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSGWAQIIGGHEVTPHSRPMASVRFGQHHCGGFLLRARWVVSAAHC
FSHRDLRTGLVVVLGAHVLSAETPQQVFGIDALTTHPDYHPMTHANDICLRLNLSAVLGPAVGLLRLPGREARP
PTAGTRCRVAGWGVSDFEELPPGLMEAKVRLDPDVNCSSWKGHILTMLCTRSGDSHRRGFCSDSGGPLVCR
NRAHGLVFSGLWC GDPKTPDVYTQVS AFVAIW DV V RSSP QPGPLPGT RPPGEAA
```

**Signal peptide:**  
amino acids 1-30

274/615

**FIGURE 273**

GAAGTTCGCGAGCGCTGGCTATGGGCTCTGGGGCGCGCTGGCGGGCTGCTGGCGGTGCTGGCGCTCGGGACAG  
GAGACCCAGAAAGGGCTGCGGCTCGGGCGACACGTTCTCGGCCTGACCAGCGTGGCGCGCCCTGGCGCCCG  
ACCGCCGGCTGCTGGGCTGCTGAGGCGGTACCTGCAGGGGGAGGAGGCGCGGTGCGGGACCTGACTAGATTCT  
ACGACAAGGTACTTTCTTGATGAGGATTAACAACACCCCTGTGGCTAACCTCTGCTTGCAATTACTCATCA  
AACGCCCTGCAGTCTGACTGGAGGAATGTGGTACATAGTCAGGAGGCCAGTGAGAACATCCGAGCTCTGAAGGATG  
GCTATGAGAAGGTGGAGCAAGACCTTCAGCCTTGAGGACCTTGAGGGAGCAGCAAGGGCCCTGATGCCGCTGC  
AGGACGTGTACATGCTCAATGTGAAAGGCTGGCCCAGGGTGTCTTCAAGAGAGTCAGGGCTCTGCCATCACTG  
ACCTGTACAGCCCCAACGGCTTTCTCACAGGGATGACTGCTTCCAAGTGGCAAGGTGGCTATGACA  
TGGGGGATTATTACCATGCCATTCCATGGCTGGAGGAGGCTGTCAGTCTTCCAGGATCTAACGGAGGTGA  
AGACAGAGGATGAGGCAAGTCTAGAAGATGCCATTGGATCACTTGGCCTTGCTTATTCAGGGCAGGAAATGTT  
CGTGTGCCCTCAGCCTCTCTCGGGAGCTTCTCTACAGGGCAGATAATAAGAGGATGCCAGGAATGCTTGA  
AATATGAAAGGCTCTGGCAGAGAGGACACCCAACCTACGTGGTAGCTGAGGCTGTCACTCCAGAGGCCAATATACCC  
ACCTGCCAGACCAGAGAACACCCACGGGCTATGTCAGACCCCTGGGTTCCAGGCCACTCTTACAGATCCCTA  
GCCCTACTGTTCTATGAGACCAATTCCAACGCCAACCTGCTGCTCCAGCCATCCGAAGGAGGTCACTCCACC  
TGGAGCCCTACATTGCTCTAACCATGACTCGTCAGTGACTCAGAGGCTCAGAAAATTAGAGAACCTTGCAAGAAC  
CATGGCTACAGAGGTCAGTGGTGGCATCAGGGAGAACAGCTTACAAGTGGAGTACCGCATCAGCAAAGTGCCT  
GGCTGAAGGACACTGTTGACCCAAAACGGTGAACCTCAACCACCGCATTGCTGCCCTCACAGGCCATTGATGTCC  
GGCCTCCCTATGCAGAGTATCTGCAAGGGTGAACATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATG  
CTACGTCACCAAGCAGCCCCCTACAGAACATGAAAGTCAGGAAACCGAGTTGCAACATTATGATCTATCTGAGCT  
CGGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTTAGGAATGCAGCACTGT  
TTTGGTGGAACCTGCACAGGAGTGGTGAAGGGAGCAGTGACACACTTCATGCTGGCTGTCCCTGGTGGAG  
ATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGGACAGGAATTCCGAGAACCCCTGCAGCTCCAGGCCCTGAAG  
ACTGAACACTGTTGGCAGAGAGAACGCTGGGAGTCTGGCTTCCAGAGAACGCCAGGAGCAGGAGCTGGGTA  
GGAGAGGAGAACAGAGCAGGCCCTGGAGAACAGGCCCTGTCAGGTTGCTGTGCCTCGCAAATCAGAGGCAA  
GGGAGAGGTTGTTACCCAGGGGACACTGAGAACATGATCTGCCCCAGCAGGAAGTCAGAGTAGGATGCA  
ACAGTACAAAGGAGGGGGAGTGGAGGGCTGAGAGGGAGTTCTGGAGTTCAAGATACTCTGTGGGAACAGG  
ACATCTAACAGTCTCAGGTTGATCAGTGGGCTTGGCACTTGAACCTTGACCAACAGGGACCAAGAACAGTGG  
CAATGAGGACACCTGCAGGAGGGCTAGCCTGACTCCCAGAACCTTAAGACATTCTCCCCACTGCCCTGCTGC  
AGCCCAAGCAGGGAGTGTCCCCCTCCCAGAACATATCCCAGATGAGTGGTACATTATAAGGATTTTTAA  
GTTGAAAACAACCTTCTTTCTTTGTATGATGGTTTTAACAGTCATTAAAATGTTATAAATCAAA

275/615

FIGURE 274

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64849
><subunit 1 of 1, 544 aa, 1 stop
><MW: 61126, pI: 6.40, NX(S/T): 2
MGP GAR LA ALL A VIAL ALG TD PER A A R G D T F S A L T S V A R A L A P E R R I L G L L R R Y I L R G E E A
R L R D L T R F Y D K V L S I H E D S T T P V A N P L L A F T L I K R I Q S D W R N V V H S I E A S E N I R A L K D G Y
E K V E Q D L P A F E D L E G A A R A L M R L Q D V Y M L N V K G L A R G V F Q R V T G S A I T D L Y S P K R L F S L T
G D D C F Q V G K V A Y D M G D Y Y H A I P W L E E A V S L F R G S Y G E W K T E D E A S L E D A L D H I A F A Y F R A
G N V S C A L S I S R E F L L Y S P D N K R M A R N V L K Y E R L I A E S P N H V V A E A V I Q R P N I P H I Q T R D T
Y E G L C Q T L G S Q P T L Y Q I P S L Y C S Y E T N S N A Y I L L Q P I R K E V I H L E P Y I A L Y H D F V S D S E A
Q K I R E L A E P W L Q R S V V A S G E K Q L Q V E Y R I S K S A W L K D T V D P K L V T L N H R I A A L T G L D V R P
P Y A E Y L Q V V N Y G I G G H Y E P H D H A T S P S S P L Y R M K S G N R V A T F M I Y L S S V E A G G A T A F I Y
A N L S V P V V R N A A L F W W N L H R S G E G D S D T L H A G C P V L V G D K W V A N K W I H E Y G Q E F R R P C S S
S P E D
```

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-19

**Leucine zipper pattern:**

Amino acids 34-56; 41-63

**Ribonucleotide reductase small subunit signature:**

Amino acids 340-356

**N-glycosylation sites:**

Amino acids 242-246; 482-486

**Cell attachment sequence:**

Amino acids 27-30

**Tyrosine kinase phosphorylation site:**

Amino acids 189-198

**N-myristoylation sites:**

Amino acids 4-10; 135-141; 153-159; 164-170; 241-247; 303-309; 309-315;  
457-463; 473-479

276/615

FIGURE 275

GGCAACATGGCTCAGCAGGCTTGC~~CCC~~CAGAGCCATGGCAAAGAATGGACTTGTAA~~TT~~GCATCCTGGTATCACC  
TTACTCCTGGACCAGACCACCAAGCCACATCAGAATTAAAGCCAGGAAGCAGC~~AA~~ACGTGAGTGAGAGAC  
AAGGATGGAGATCTGAAGACTCAAAATTGAAAGCTCTGGACAGAAGTCATGCCTGAAGGAAATTCAAGCCCTG  
CAGACAGTCTGTCTCCGAGGGACTAAAGTCACAAGAAAAGCTACCTGCTCAGAAGGTTGAAGGCATTCCAT  
GAGGCCAATGAAGACTGCATTCCAAAGGGAGGAATCCTGTTATCCCCAGGAACTCCGACGAAATCAACGCCCTC  
CAAGACTATGGTAAAGGAGCCTGCCAGGTGTCATGACTTTGGCTGGCATCAATGACATGGTACCGGAAGGC  
AAGTTGTTGACGTCAACGGAATCGCTATCTCTCCTCACTGGGACCGTGCACGGCTAACGGTGGCAAGCGA  
GAAA~~ACT~~TGTCTCTGTCAGCTCAGGGCAAGTGGAGTGTGAGGCCGTGCGCAGCAGCAAGAGATA  
ATATGCGAGTTCACCATCCCTAAATAGGTCTTCTCAATGTGTCTCCAAGCAAGATT~~CAT~~CATAACTTATAGG  
TTCATGATCTAAGATCAAGTAAAATCATAA~~TTT~~ACTTATTAAAAAAATGCAACACAAGATCAATGTCAT  
AGCAATATGATAGCATCAGCCAATTGCTAACACATTCTTGGGATTTGCCCTCCTGGGTATAGGGGATC  
AGAAAATATTGATCCATGTGCACGCA~~GATAAA~~ATGGCTCTGCTAACAGACTAAATCTCTAGTCTTC  
TCACITGACAAACCCAGTTGTTCAAAAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTT  
AGGCTACCTGAAAGATTCCCTTGGAGTTAGCGTATGTTGACTAACAAAATCCCTACATCAGAGACTCT  
AGGTGCTATATAATCCAAA~~ACT~~TTTCAGCCTGCTCATCTCTGGGACTTGTATCTGCTGCCATATCAGAACACAAACCC  
CAATTACCCCTATTGAAATTGCTCATCTCTGGGACTTGTATCTGCTGCCATATCAGAACACAAACCC  
TGAAGAGGTTCTGATTGATTTTTTTCTCATGCC~~TAC~~CTTTGGAGTTCCAGCCGAATTG  
AATGAAATGACAAGGTGATATTGATCAATTTCATTCCACCATTGCAATTACACCTCTAACCTAAATGGCTA  
ACCCTAAGGCATATCAAAGAAGCAGATTGCA~~GATAA~~ACGGAAATGAGAAAAAGAACCTACATTATTTGCTT  
TAGCATCCTTACTCTCACCTTATGAGATTGAGAGTGGACTTACATTCCCTTTACATTTCGTATATT  
TTTTTTAGCCATCATTATGTTAAGTCTATTATGGCAACCAATTGGAGCTGAAA~~ACT~~GAATTAAAG  
AATGCTATCTGGAAAATTGCACTCGTGTGCAATT~~TTT~~ATTCTGCC~~TAG~~TGCTATTCTGCTTAACTAG  
ATTGTACAAAATAACTCATTGCTTAATATCAAATTACAAAGTTAGACTTGGAGGGAAATGGCTTTAGAAG  
CAAACAAATTAAATATTGTTCTCAAAATAATAGTGTAAACATTGAATGTGTTTAGCTGTTTCAATTGCTCAAA  
CACTTTGCAA~~ACT~~TTA~~ACT~~ACACATGCTGGAA~~TTAAGT~~TTAGCTGTTTCAATTGCTCAAAATAAGCCTGAA  
TTCTGATCAATaaaaaaaaaaaaaaaaaaaaaaa

277/615

FIGURE 276

MAQQACPRAMAKNGLVICILVITLLLQTTSHTSRLKARKHSKRRVRDKDGDLKTQIEKLWTEVNALKEIQALQT  
VCLRGTKVHKCYLASEGLKHFEANEDCISKGGILVIPRNSDEINALQDYGKRSLPGVNDFWLGINDMVTEGKF  
VDVNGIAISFLNWDRDRAQPNGGKRENCVLFSQSAQGKWSDEACRSSKRYICEFTIPK

278/615

FIGURE 277

GAGATAGGGAGTCTGGGTTAAGTCCTGCTCCATCTCAGGAGCCCCCTGCTCCACCCCTAGGAAGCCACCAGAC  
TCCACGGGTGCGGGCCAATCAGGTGGAATCGGCCCTGGCAGGGCAGAGCCTGGCTGAGGGACCGAGCC  
GGAGAGCCCCGGAGCCCCCGTAACCCGCGGGGGAGCAGGATTCCCGCAGGGGACTCGGAGCAGGTGCGCT  
ACTGCGCGCCTTCTCCTACCTCTGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGG  
CCCTGGTCTGTCTGGCATCTATGCAAGAGGTTGAGCGCAGAAATAAAACCTTGAAAGTGCCCTCTGG  
CTCCAGCATCATCCTCATCCTCTGGCGTGTATGGTATGCTCTCCCTATTGGTGTGCTGGCGTCCCTCC  
GTGACAACCTGTACCTTCTCCAAGCATTGATCATGACATCCTGGGATCTGCCTCATCATGGAGCTCATTGGTGGCG  
TGGTGGCCTTGACCTCCGGAACCAGACCAATTGACTCCTGAACGACAACATTGAAGAGGAATTGAGAACTACT  
ATGATGATCTGGACTCAAAAACATCATGGACTTGTTCAGAAAAGTCAAGTGCTGTGGCGGGGAGGACTACC  
GAGATTGGAGCAAGAATCAGTACCAACGACTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC  
GCATCAGGAACACGACAGAAGTTGCAACACCATGTTGGCTACAAACTATGACAAGGAGCCTTCAAGTGTGC  
AGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCATCTGGTTCATGACAACACTACACCATCATGGCGT  
GCATCCTCTGGCATCCTGCTCCCCAGTCTGGGGGTGCTGCTGACGCTGTCATCACCCGGGGTGGAGG  
ACATCATCATGGAGCACTCTGCACTGATGGCTCTGGGGCTGGCAAGCCCAGCGTGGAGGCGCAGGCA  
CGGGATGCTGCTGTGCTACCCAAATTAGGGCCAGCCTGCCATGGCAGCTCAACAAAGGACCGTCTGGGATAGC  
ACCTCTCAGTCACATCGTGGGGCTGGACAGGGCTGCGGCCCCCTGCCCACACTCAGTACTGACCAAAGGCCAGG  
GCTGTGTGTGCTGTGCTAGGTCCCACGGCTCTGCCTCCCCAGGGAGCAGGCCTGGGCTCTCCCTAAGAGGC  
TTTCCCCAGGGCAGCTGGAATCTGTGCCACCTGGGGCTGGGAACAAGGCCCTCCTTCTCCAGGCCCTGG  
CTACAGGGGAGGGAGAGCCTGAGGCTCTGCTCAGGGCCATTTCATCTCTGGCAGTGCCTGGCGGTGGTATTCA  
AGGCAGTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCCTGGGGCAGGAGGGAGGGCATCTGGGAA  
GGCAGGAGGGAAAGAGCTGTCCATGCAGCCACGCCATGGCAGGTGGCCTCTCAGCCTCCAGGTGCC  
GAGCCCTTGCAAGGGCGGCTGCTTCCITGAGCCTAGTTTTTACGTGATTTTGTAAACATTCAATT  
GTACAGATAACAGGAGTTCTGACTAATCAAAGCTGGTATTCCCGCATGTCCTATTCTGCCCTCCCCAAC  
CAGTTGTTAACAAACAATAAAACATGTTTGTGTTAAAAAA

279/615

**FIGURE 278**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863  
><subunit 1 of 1, 294 aa, 1 stop  
><MW: 33211, pI: 5.35, NX(S/T): 3  
MPRGDSEQVRYCARFSYLWLKFSLIIYSTVFWLIGALVLSVGIFYAEVERQKYKTLESAFLAPATIILILLGVVMFM  
VSFIGVLASLRDNLYILLQAFMYILGICLIMELIGGVVALTFRNQTIDFLNDNIRRGIEYYDDLDFKNIMDFVQK  
KFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCCIRNTTEVVNTMCGYKTIDKERFSVQDVYVRGCTNAVII  
WFMDNYTIMACILLGILLPQFLGVLLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCLCYPN

**Signal peptide:**  
amino acids 1-44

**Transmembrane domains:**  
amino acids 22-42, 57-85, 93-116, 230-257

280/615

**FIGURE 279**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCCAGGTCTGCATCCTGCACTTGCTGCCCTCTGACACCTGGGAAGAT  
GGCCGGCCCCGTGGACCTTCACCCCTCTGTGGTTGCTGGCAGCCACCTTGATCCAAGGCCACCCCTCAGTCCCAC  
TGCAGTTCTCATCCTCGGCCCCAAAGTCATCAAAGAAAAGTCAGACAGGAGCTGAAGGACACAACGCCACCAG  
CATCCTGCAGCAGCTGCCGCTGTCAGTGCAGCTGGGAAAAGCCAGCCGGAGGACATCCCTGTGCTGGCAGCCT  
GGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCAACAGCTAACATCCTCCAGCTGCAGGTGAAGGCC  
CTCGGCCATGACCAGGAGCTGCTAGTCAGATCCCCCTGGACATGGTGGCTGATTCAACACGCCCTGGTCAA  
GACCATGTTGGAGTTCACATGACGACTGAGGCCAAGCCACCATCCGCATGGACACCCAGTGCAGTGGCCAC  
CCGCCTGGCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAACGTGTATAAGCTCTCCTTCT  
GGTGAACGCCCTAGCTAACGAGGTCAACCTCTAGTGCCATCCTGCCCATCTAGTGAAAAACAGCTGTG  
TCCCCTGATCGAGGCTCCTCAATGGCATGTATGCAGACCTCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAG  
CATTGACCGTCTGGAGTTGACCTTCTGTATCCTGCCATCAAGGGTGAACACCATTAGCTCACCTGGGGCCAA  
GTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTCAATAACTCTGCAGTCCCTGACAAATGCCACCCCTGGA  
CAACATCCCGTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGGCTGCAGTGGCTGCTGTGCTCTCCAGAAGA  
ATTCACTGGTCTCTGGGACTCTGTGCTTCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGA  
AAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTTTTTATAGA  
CCAAGGCCATGCCAAGGTGGCCAACTGATCGTGTGGAAAGTGTTCCTCCAGTGAAGGCCCTCCGCCCTTGT  
CACCCCTGGCATTGAGCCAGCTCGGAAGCTCAGTTTACACCAAGGTGACCAACTTAACTCAACTTGAATAA  
CATCAGCTCTGATGGATCCAGCTGATGAACCTGGGATTGGCTGGTCAACCTGATGTTCTGAAAAACATCAT  
CACTGAGATCATCCACTCCATCCTGCTGCCAACAGAATGGCAAATTAAAGATCTGGGTCCAGTGTGATTGGT  
GAAGGCCTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGCTTACTCCAGCCTCTTGT  
GAAACCCAGCTCTCCTGTCCTCCAGTGAAGACTGGGATGGCAGCCATCAGGGAGGCTGGTCCCAGCTGGGAGT  
ATGGGTGTGAGCTATAGACCATCCCTCTGCAATCAATAAACACTTGCTGTGAAAAA

281/615

**FIGURE 280**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881  
><subunit 1 of 1, 484 aa, 1 stop  
><MW: 52468, PI: 7.14, NX(S/T): 3  
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPVKVKEKLTQEIKDHNATSILQQLPLLSAMREKPAGGIPVLGS  
LVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVEFHMTTEAQATIRMDTSASGP  
TRLVLSDCATSHGSIRIQLLYKILSFLVNALAKQVMNLLVPSLPNVLKNQLCPVIEASFNGMYADLLQLVKVPISL  
SIDRLEFDLLYPAIKGDTIQQLYLGAKLDSQGKVTKWFFNSAASLTMPTLDNIPFSLIVSQDVVKAAVAAVLSPE  
EFMVLLDSVLPSAHLRKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSEALRPL  
FTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIHSILLPNQNGKLRSGVPVSL  
VKALGFEEAAESSLTKDALVLTPASLWKSSPVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

282/615

FIGURE 281

CCCCACGCGTCCGCCTCTCCCTCTGCTGGACCTTCCTCGTCTCCATCTCTCCCTCCTTCCCCGCCTCT  
CTTTCCACCTTCTCTTCTTCCACCTTAGACACTCCCTCGCCCTCTTCCGCCCCACCGCTGCTTCCCTGGC  
CCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCCTGGGGTCTGTGGGGTGTATCTGTGGCCCCCTGTGCCTCCGTGTC  
CTTTCTCGCTCCCTCTCCCGCTCCGCTCCGGACCAGGGCCCTGACCCCTGGGGAAAGG**ATGG**TGTTCCCGAGGT  
GAGGGTCCCTCTCCCTCTGGGACTCGCGCTGCTCTGGTCTCCCTGGACTCCACGCTCGAGGCCGCCAGA  
CATGTTCTGCTCTTCCATGGGAAGAGATACTCCCCCGGGAGAGCTGGCACCCCTACTTGGAGGCCACAAGGCCT  
GATGTAAGTCTGCTCGCTGTACCTGCTCAGAGGGCGCCATGTGAGTTGTTACCGCCCTCCACTGTCCGCTGTCCA  
CTGCCCCCAGCGTGTGACGGAGCCACAGCAATGCTGTCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCG  
GGCCCCCACAAAGTCTGCCAGCACACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCAGTGACTGTT  
CCCCCTCCCGCTGCCAACAGTGTGTCTGCAAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACACCTG  
CCCCGAACCAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAACGCTGCAAAGATGAGGCAAGTGA  
GCAATCGGATGAAGAGGGACAGTGTGCACTCGCTCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGC  
TGGGAGAAAGAGAGGGCCGGGACCCAGCCCCACTGGCCTCAGGCCCTCTGAGCTTCATCCCTGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACACTGTCAAGATGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTCATGG  
CGGGAAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCTGCCCTGCCCCCTGCCCTGCATCCTATG  
CACCTGTGAGGAGATGGCCGCCAGGACTGCCAGCTGTGACCTGTGCCCCACCGAGTACCCCTGCCGTACCCCGAGAA  
AGTGGCTGGGAAGTGCTGCAAGATTGCCCCAGGGACAAAGCAGACCCCTGGCCACAGTGAGATCAGTTCTACCA  
GTGTCCCCAAGGCACGGGCCGGTCTCGTCACACATCGGTATCCCCAAGGCCAGACAAACCTGCCGTGCTTTC  
CCTGGAACACGAGGCCTGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCA  
GAGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAATCTTCAACTGACTCAGATCAAGAAAGTCAGGAAGC  
AAGACTTCCAGAAAGAGGGCACAGCACTCCGACTGCTCGCTGGCCCCACGAAGGTCACTGGAACGTCTCCTAG  
CCCAGACCCCTGGAGCTGAAGGTCA CGGCCAGCCAGACAAAGTGACCAAGACATAACAAAGAC**TAACAGTTGCA**  
GATATGAGCTGTATAATTGTTGTATTATATATTAAATAAGAAGTTGCATTACCTCAAAAAAAA  
AAAAAAA

283/615

FIGURE 282

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRLSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSEGAHVSCYRLH
CPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELFPSRLPNQCVLCSCTEGQIYC
GLTTCPPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVRHPQDPCSSDAGRKRGPFTPAPTGLSAPLSF
IPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPC
RHPEKVAGKCKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDE
ETEAQRGEVPGPRPHSQNLPLSDQESQEALPERGTALPTARWPPRSLERLPSPDPGAEGHGQSRQSDQDITKT
```

**Signal peptide:**  
amino acids 1-25

284/615

**FIGURE 283**

GGCATGGTGCGCCCGTGGCGGTGGCGGCCGGTGGCGGAGGCTTCCTGGTCGGATTGAAACGAGGAGAAGAT  
GACTGACCAACCAGACTGGCTGAATGAATGAATGGCGGAGCCAGCGCGCCATGAGGAGCCTGCCGAGCTGGCG  
GCCCTGCCCTGTTGCTGCCGCCGCCGCCGCCGCGCTGCCCTCAGCCGCCCTGCCGGGGGAATGTACCCGGTG  
GGGGCGGGGCCGCCGGGGCACGTGGACCGCTGCCGGGCCGGGGTGCAGGGGCCAGGCCACCCCTCCCTA  
GGGCAGGGCTCCCACGGCCCCAGGGCCCCAGGGACCGGGCCCCGCCGCCACCGTCCACCAGCACCCCTGGCTGC  
CTTCTCCAGCCCCAGTCCCCGGAGACCACCCCTTTGGCGACTGCTGGACCCCTTCCACACCTTCAAGGCC  
CGCTCGGCCCCCTGCCGCCACCCCTCCGGCGGCCAACGCACTTCGACCACCTCTCAGGCCGACCAGACCCG  
CGCCGACCAACCCCTTCGACGACCAACTGGCCCGCGACCACCCCTGTAGCGACCACCGTACCGGCCACAGA  
CTCCCCGGACCCCGACCCCCGATCTCCCCAGCAGCAACAGCAGCGTCCTCCCCACCCACCTGCCACCGAGG  
CCCCCTCTCGCTCTCCAGAGTATGTATGTAAC TGCTCTGTGGTGGAAAGCCTGAATGTAATCGCTGCAACC  
AGACCACAGGGCAGTGTGAGTGTGGCCAGGTTATCAGGGGCTTCACTGTGAAACCTGCAAAGAGGGCTTTTAC  
TAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGTAGTCCACATGGAGCTCTCAGCATAACCGTGCAACAGGT  
AAGCAACAGAGGGTGAACGTGAAGTTATTTATTTAGCAAGGGAAAAAAAAGGCTGTAACCTCAAGGACCA  
TACTGGTTAAACAAGGAGGATGAGGGTCA TAGATTACAAATATTTATATACTTTATCTTACTTTATCTTACTTTAT  
ATGTTATTTAATGTCAGGATTAAAAACATCTAATTACTGATTAGTTCTCTCAAAAGCACTAGACTCGCCAA  
TTTTCTCTGGGATAATTCGTAATTTCATGGAAAAAAATTATTGAAGAATAAAATCTGCTTCTGGAGGGCT  
TTCAGGCATGAAACCTGCTAGGGGTTAGAAATGTTCTATGTTATTAATACCATTTGAGGTTGGAGGAAAT  
TTGTTGTTGGTTATTTCTCTTAATCAAATCTACATTGTTCTTGACATCTAAAGCTTAACCTGG  
GGTACCCCTAATTATTAATTAACAGTGGTAACTAGACTGGTTTACTCTATTACAGTACATTGGAGACCAAA  
GTAGATTAAGCAGGAATTATCTTAAACTATTATGTTATTGGAGGTAAATTAAATCTAGTGAATAATGACTGT  
TATCTAAGCAATTGCTTGTACTGCACTGAAAGTAATTATTCTGACCTTATGTTGAGGCACTGGCTTTGTG  
GACCCCAAGTCACAAAAGTGAAGAGACAGTTAAATAATGAAAAAAATAATGACAGGTTACTCAGTGTAA  
TGGGTATAACCAAGATCTGCTGCCACTTACGAGCTGTTCTGGCAAGTAATTCTTCACTGAGCTTGT  
TTCTCTCAAGGTTGTGAAGATTAAATGAGTTGATATATAAAATGCCTAGCACATGTCACTCAATAAATT  
CTGGTTGTTTAATTCAAGGAATATTATGGACTGAAATGAGAGAACATGTTTAAGAACTTTAGCTCCCTG  
ACAAAGAAGTGCTTTATACTTAGCACTAAATATTAAATGCTTATAAAATGATATTACTGTTATGGAATAT  
TGTATCATATTGTAGTTATTAAAATGTAAGAAGAGGCTGGCGCGGTGGCTCACGCCGTAACTCCTAGCACTTT  
GGGAGGCAAGGCCGGGGATCACTTGAGGGCAGGAGTCTAGATGAGCCTGGCCAGCACAGTGAACCCCCGTCT  
CTACTAAAAAATACAAACAAATTAGCTGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC  
AGGAGAATCGTTGAACCCGGGAGGTGGAGGTTGCACTGAGCTGAGATCGCGCACTGCACTCCAGCCTGGTGAG  
AGAGGGAGACTCTGCTTAAAAAAAAAAAAAA

285/615

FIGURE 284

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSILPSLGGIALLCCAAAAAAVASAASAGNVGGGAAGQVDASPGPGLRGEPSHPFPRATAPTAQAPRTGPPRA
TVHRLPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTTPPAERTSTTSQAPTRPAPTLSTTGPAPTTPV
ATTVPAPTTPRTPTPDLPSSNSVLPTPPATEAPSSPPPEYVCNCVVGSLSNVRCNQTTGQCECRPGYQGLHC
ETCKEGFYLNYSGLCQPCDCSPHGALSIPCNR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

286/615

**FIGURE 285**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCAACCCCAGACATGCTGCTGCTGCCCTGCTCTGGGG  
AGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCGTGACGGTCAGGAAGGCTGTGT  
GTCCATGTGCCCTGCTCCTCTCCATCCCCCTCGCATGGCTGGATTACCCCTGGCCAGTAGTTCATGGCTACTGG  
TTCCGGGAAGGGGCCAATACAGACCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGAGGAG  
ACTCGGGACCGATTCCACCTCCTGGGGACCCACATACCAAGAATTGACCCCTGAGCATCAGAGATGCCAGAAGA  
AGTATGCGGGGAGATACTTCTTCGTATGGAGAAGTAATAAAATGGAATTATAAACATCACCGCCTCTCT  
GTGAATGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCCAGGCACCCCTGGAGTCCGGCTGCCCTCAGAAT  
CTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCTGGATAGGGACCTCCGTGTCC  
CCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGTCACCCCTCATCCCACAGCCCCAGGACCATGGCACCCAGCCTC  
ACCTGTCAGGTGACCTTCCCTGGGGCAGCGTGACCAAGAACAGACGTCCATCTAACGTGTCCTACCGCCT  
CAGAACTTGACCATGACTGTCTCCAAGGAGACGGCACAGTATCCACAGTCTTGGAAATGGCTCATCTGTCA  
CTCCCAGAGGGCCAGTCTCGCCCTGGTCTGTGAGTTGACAGTGTGACAGCAATCCCCCTGCCAGGCTGAGC  
CTGAGCTGGAGAGGCCTGACCCCTGTGCCCTCACAGCCCTCAAACCCGGGGTGTGGAGCTGCCCTGGGTGCAC  
CTGAGGGATGCAAGCTGAATTCACCTGCAGAGCTCAGAACCCCTCTGGCTCTCAGCAGGTCTACCTGAACGTCTCC  
CTGCAGAGCAAAGCCACATCAGGAGTGAATCAGGGGGTGGTCAGGGGGAGCTGGAGCCACAGCCCTGGCTTCCCTG  
TCCTTCTCGCTCATCTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAGGCCAGCAGGGGGCTGGAGAT  
ACGGGCATAGAGGATGCAAACGCTGTCAAGGGGTTCAAGCCTCTCAGGGGCCCTGACTGAACCTTGGGAGAAC  
AGTCCCCAGACCAGCCTCCCCCAGCTCTGCCCGCTCTCAGTGGGGAGGGAGGAGCTCCAGTATGCACTCC  
AGCTTCCAGATGGTGAAGCCTGGGACTCGGGGGACAGGAGGCCACTGACACCGAGTACTGGAGATCAAGATC  
CACAGATGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCAAGAGC  
TGATTCTGTAGAATTAAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATGTGCAGAGTGAAGA  
ACACAGGCTTCTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCCTCCCTTATTTTTAACAAAAG  
ACAGACAAATTCTCA

287/615

**FIGURE 286**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTQEGLCVHVPSCFSYPSHGWIYPGPVVGWREGANTDQDAPVA  
TNNPARAVWEETRDRFHLLGDPTHKNCTLISRARRSDAGRYFFRMEKGSIKWNYKHHRLSVNVTALTHRPNILI  
PGTLESGCPQNLTCSVWACEQGTPPMISWIGTSVSPLDPSTTRSSVTLIPIPQPDHGTSILTCQVTFPAGSVTTN  
KTVHLNVSYPPQNLMTMVFQGDTVSTVLNGNSSLSLPEGQSLRLVCAVDADSNPPARLSLSWRGLTLCPSQPS  
NPGVLELPWVHLRDAEFTCRAQNPLGSQQVYNVSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRK  
KSARPAAGVGDTGIEDANAVRGSAASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOQYASLSFQMVKPWDSRGQE  
ATDTEYSEIKIHR

**Signal peptide:**  
amino acids 1-15

**Transmembrane domain:**  
amino acids 351-370

288/615

**FIGURE 287**

CGCGAGCTGAGAGGGAGCAGGTAGAGGGGAGGGCGGGACTGTCGTCTGGGGAGCCGCCAGGAGGCCTCTCAG  
GCCGACCCAGACCCCTGGCTGGCAGGATGAAGTATCTCCGGCACCGGCCAATGCCACCCCTCATCTGGCC  
ATCGGCGCTTCACCCCTCCCTCAGTGTCTAGTGTCAACCACTGCAAGGTCCAGGAGCAGCCACCG  
GCGATCCCCGAGGCCCTGGCTGGCCACTCCACCCACCCAGGGCCCGTGCATGCCAACACCTCT  
ATGGTCACCCACCCGACTTCGCCACGCAGCCGAGCACGTTCAAGAACCTCCTCTGTACAGACACTGCCGCAC  
TTTCCCCTGCTGAGACGTGCCAGCGAGCTGCTGCCAGCAGTGGGCGAGCGCAAGGTACGGGTTTGCAAGCTG  
CCTAGCAACTATGTGCCGCCGAGCTGCTGCCAGCAGTGGGCGAGCGCAAGGTCAACCGGTGCTGGAGCTGGAG  
GCACAGACTCACGGAGACATCTGCAGTGGACTTCACGACTCCTCTCAACCTCACGCTCAAGCAGGTCTG  
TTCTTACAGTGGCAGGAGACAAGGTGCGCAACGCCAGCTCGTGTCAACGGGATGATGACGTCTTGACAC  
ACAGACAACATGGCTTCTACCTGCAAGGACATGACCTGGCCACCTCTCGTGGGCAACTGATCCAAAAC  
GTGGGCCCCATCCGGCTTTTGAGCAAGTACTATGTGCCAGAGGTGGTGACTCAGAAATGAGCGGTACCCACCC  
TATTGTGGGGGTGGCTGGCTCTTGCTGTCCCCTCACGGCGCTGCCCTGCCGCTGCCATGTCCTGGAC  
ATCTCCCCATTGATGATGTCCTCTGGGTATGTCCTGGAGCTTGAGGGACTGAAAGCTGCCCTCCCACAGCGGC  
ATCCGCACGTCTGGCGTGCCTCCATCGAACACCTGCTCCCTTGACCCCTGCTTCAACCGAGACCTGCTG  
CTGGTGCACCGCTCCTACCTATGAGATGTCATGTCATGGGATGCGCTGAACCAGCCCAACCTCACCTGCC  
AATCAGACACAGATCTACTGAGTCCAGCATCAGGTCCCCAGCCTGGCTCTGTTCCATAGGAAGGGGCGAC  
ACCTCCCTCCAGGAAGCTTGTGGTCTGAGCATAAGGGAGTGCCAGGGAGGTTGAGGTTGATGA  
GTGAATATTCTGGCTGGCAACTCCTACACATCCTCAAAACCCACCTGGTACTGTTCCAGCATCTCCCTGGAT  
GGCTGGAGGAACCTCAGAAAATATCCATCTCTTTGTGGCTGCTAATGGCAGAAGTGCCTGTGCTAGAGTCC  
AACTGTGGATGCATCCGTCCCGTTGAGTCAAAGTCTTACTTCCCTGCTCACCTACTCACAGACGGGATGCTA  
AGCAGTGCACCTGCAGTGGTTAATGGCAGATAAGCTCCGTCTGCAGTCCAGGCCAGCCAGAAACTCCGTGTC  
CACATAGAGCTGACGTGAGAAATATCTTCAGCCCAGGAGAGAGGGGTCTGATCTAACCTTCTGGGTCTC  
AGACAACTCAGAAGGTTGGGGGATACCGAGAGAGGGGGAGGCAAGTGTCTTGAAAGTTGTGAGAGGCTCAGAGTTCTG  
ATGCTGTAATGGTGGAGGTGTGGCAGAGGAGGGAGGCAAGTGTCTTGAAAGTTGTGAGAGGCTCAGAGTTCTG  
GGGTCTCATTAGGAGCCCCCATCCCTGTTCCCAGAATTAGAGAACAGCACTGGGCTGGAATGATCTT  
AATGGGCCAAGGCCACAGGCATATGCCCTCACTACTGCCCTGGAGAGAGGGAGAGATTAGGTCTCCAGCAGCCT  
CCCTCACCCAGTATGTTACAGATTACGGGGGACCGGGTGAGCCAGTGACCCCTGCAGCCCCCAGCTCAGG  
CCTCAGTGTCTGCCAGTCAGCTCACAGGCAATTGTGATGGGCAGCCTGGGAATATAAAATTGTAAGAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

289/615

**FIGURE 288**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65413
<subunit 1 of 1, 372 aa, 1 stop
<MW: 42515, pI: 8.92, NX(S/T): 6
MKYLRHRRPNATLILAIGAFTLLLFSLLVSPPTCKVQEQQPAIPEALAWPTPPTRPAPAPCHANTSMTHPDFAT
QPQHVQNFLLYRHCRHFPLLQDVPPSKCAQPVFLLLVIKSSPSNYVRRELLRRTWGRERKVGRGLQLRLLFVGTA
SNPHEARKVNRLLELEAQTHGDIQWDFHDSFFNLTLKQVLFLQWQETRCANASFVLNGDDVFAHTDNMVFYLQ
DHDPGRLFVGQLIQNVGPIRAFWSKYYVPEVVTQNERYPPYCAGGGFILLSRFTAALRRAHVLIDFPIDDVFL
GMCLELEGKLPASHSGIRTSGVRAPSQHLSSFDPCFYRDLLLVHRFLPYEMLLWDALNQPNLTCGNQTQIY
```

**Important features:****Type II transmembrane domain:**

Amino acids 15-34

**N-glycosylation sites:**

Amino acids 10-14; 64-68; 184-188; 202-206; 362-366; 367-371

**TonB-dependent receptor proteins signature 1:**

Amino acids 1-32

**N-myristoylation sites:**

Amino acids 308-314; 316-322

290/615

**FIGURE 289A**

CGGGCTCCCCGGCCCTCCCTGGGCTCCACGGTCTTCCCCGAGAGGCAGCCCTCCTCCAGGAGCGGGCCCT  
GCACACCATGGCCCCGGGTGGCAGGGGTGGCGCCGGCTGCGCCGCCCTGGCGCTGGCCTTGGCGCTGGC  
GAGCGTCTTGAGTGGCCTCCAGCCGTGCGCTGCCCCACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCA  
CGGGCTGGGCTCCGCGGGTCTCGGGCATCCCCCGAACGCTGAGCGCCTTGACCTGGACAGAAATAATAT  
CACCAAGGATCACCAAGATGGACTCGCTGGCTCAAGAACCTCGAGTCITGCACTGGAAAGACAACCAGGTCA  
CGTCATCGAGAGAGGGCCTTCAGGACCTGAAGCAGCTAGAGCAGTGCCTGAACAAGAATAAGCTGCAAGT  
CCTTCCAGAATTGCTTTCCAGAGCACGCCAACGCTACCCAGACTAGATTTGAGTGAAGAACCTGCAACTGG  
ACAACAACCACATCAGCTGCATTGA  
CCCAGGAAAGCGTCCGCGCATCACCGATGTGAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGA  
AGATGGAGCCTCCGAGCGTGCAGATTGGAGATCCTTACCCCTAACAAACAACATCAGTCGCATCCTGGT  
CACCAAGCTCAACCACATGCCGAAGATCGAACTCTGCCTCCACTCCAACCACCTACTGCACTGCCACCT  
GGCCTGGCTCTCGGATGGCTGCAGCGACGGACAGTTGGCAGCTCACACTCTGCATGGCTCCTGTGCATT  
GAGGGGCTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTGTGCCCCAGCCCCCACTCGGAGGCCCCATCCTG  
CAATGCCAACCTCCATCTGCCCTGCACGTGAGCAATAACATCGTGGACTGTGGAGAAAGGGCTT  
GATGGAGAATCTGCCAACCTGCCGGAGGGCATCGTGAAGAACCTGCTAGAACAGAACCTCATCAAAGC  
TGCAGGAGCCTCACCCAGTACAAGAACCTGCAAGAACATCGAGTGGATATTGGGATATTGCTCC  
AGATGCCTCCAGGGCCTGAAATCACTCACATCGTGGCTGTATGGGAAAGATCACCGAGATTGCCAACGG  
ACTGTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCTCAATGCCAACAGATCAACTGCCTGCAGGGTGAACAC  
GTTTCAGGACCTGCAGAACCTCAACTTGCTCCTCTGTATGACAACAAGCTGCAGAACCATCAGCAAGGGCTT  
CGCCCTCTGCAGTCCATCCAGACACTCCACTTAGCCAAAACCCATTGTTGCGACTGCCACTGAAGTGGCT  
GGCGACTACCTCCAGGACAACCCATCGAGACAAGCGGGCCGCTGCGAGCAGCCCGCAGCAGCAG  
GCGCATGCCAGATCAAGAGCAAGAAGTCCGCTGCTCAGGCTCCGAGGATTACCGCAGCAGGTT  
GTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCTGTGAGGGCACGATTGTGGACTGCTCCAACCAG  
GGTCCGCATCCCAAGOCACCTCCUTGAATATGTCACCGACCTGCACTGAATGACAATGAGGTATCTGTTCTGG  
GGCCACTGGCATCTTCAAGAAGTGGCCAAACCTGCGGAAATAATCTGAGTAACAATAAGATCAAGGGTGC  
AGAGGGAGCTTCGATGGAGCAGCGTGCAGGAGCTGATGCTGACAGGGAACCGAGTGGACTGCTGCCAG  
GCGCGTGTCCGTGGCTCAGTGGCCTCAAAACCTGTATGCTGAGGAGTAATTGATCAGCTGTGAGTAATGA  
CACCTTGGCGGCTGAGTCGGTGAGACTGCTGCTCCTCTATGACAATCGGATCACCACATCACCCTGGG  
CTTCAACCACGTTGTCCTCCCTGTCACCATAAACCTCTGTCCAACCCCTCAACTGCAACTGCCAC  
GCTCGGCAAGTGGTTGAGGAAGAGGCGGATGTCAGTGGGAAACCTAGGTGCCAGAACGCCATT  
GATTCCCACCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAGTAGCTGCCAG  
GCGCTGCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCAGCAACAAGGGCTCCGCGCCCT  
AGGCATGCCAACGGATGTGACCGAGCTGTACCTGGAGGAAACCACCAACAGCCGTGCCAGAGAGCTGCC  
CCTCCGACACCTGACGCTTATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCA  
GTCTCACCTCTCCACTCTGATCCTGAGCTACAAACCGGCTGAGGTGCATCCCCGTCACGCC  
GTCCTCGGAGGTGCTAACCTCCATGGCAATGACATTTCAGCGTCTCTGAAGGGCTCTCAACGCC  
TCTTCCCACCTCTGGCGCTGGGAACCAACCCACTCCAGTGTGACTGCAGTCTCGGTGGCTG  
GGCGGGGTACAAGGAGCCTGGCATGCCCGCTGCACTAGCCCTGAGCCCATGGCTGACAGGG  
CCCCAACCAACGCTTCAGTGCAGAACGGCCAGTGGACATCAACATTGTCAGGCAAT  
CCCCGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCCTGCC

291/615

**FIGURE 289B**

TACAGCTACAAGGGCAAGGACTGCCTGTGCCATCACACCTGCATCCAGAACCCCTGTCAGCATGGAGGCACC  
TGCCACCTGAGTGCACGCCACAAGGAATGGGTCAGCTGCTCCTGCCCTCTGGGCTTGAGGGCAGCGGTGTGAG  
ATCAACCCAGATGACTGTGAGGACAACGACTGCGAAAACATGCCACCTGCGTGGACGGGATCAACAACATACGTG  
TGTATCTGCCGCTTAACACACAGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTCCTGAGCTGAACCTC  
TGTCACTGAGGCCAAGTGCATCCCCCTGGACAAAGGATTCACTGAGCTGCGAGTGTGCTCTGGCTACAGCGGGAAAG  
CTCTGTGAGACAGACAATGATGACTGTGTCGGCCACAAGTGCCGCAACGGGCCAGTGCCTGAGACACAATCAAT  
GGCTACACATGCACCTGCCCTCAGGGCTTCAGTGGACCCCTCTGTGAAACACCCCCCACCCTGGCTACTGCAG  
ACCAGCCCATGCGACCAAGTACGAGTGCAGAACGGGCCAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGC  
TGCCACCAGGCTTCGCCGGCCCCAGATGCGAGAACGCTCATCACTGTCAACTCTGTGGCAAAGACTCCTACGTG  
GAACCTGGCTCCGCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCACTGACAAGGACAACGGCATT  
CTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCTGGAGACAGTGAATGATGGCAGTTCACAGTGTGGAGCTGGT  
CTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGAATGATGGCAGTTCACAGTGTGGAGCTGGT  
ACGCTAAACCAGACCCCTGAACCTAGTAGTGGACAAAGGAACCTCAAAGAGCCTGGGAAGCTCCAGAACAGCAGCCA  
GCAGTGGGCATCAACAGCCCCCTTACCTGGAGGACATCCCCACCTTACCTGGCCCTTGCAGGCCAGGG  
ACGGACCGGCTCTAGGGCGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAAACGAGCTGCAGGACTCTCAAG  
GCCCTCCACACAGTCCCTGGGGTGTCACTGGAGGCTGCAAGTCTGCACCGTGTGCAAGCACGGCTGTGCC  
TCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCAGGCCAGGCTGGACCGGCCACTCTGCAGACCAGGAGGCC  
GACCCCTGCCCTGGCACAGATGCCACCATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCC  
GAGGGCTATGGAGGGACTTGTGTGACAACAAGAACATGACTCTGCCATGCCCTGCTCAGCCTTCAAGTGTCAAC  
GGGCAGTGCCACATCTCAGACCAAGGGAGCCTACTGCCCTGCGCAGCCGGCTTAGCGGGAGCAGTGC  
CAAGAGAACCCGTGCTGGGACAAGTAGTCCGAGAGGTGATCCGCCAGAAAGGTTATGCATCATGTGCC  
GCCTCCAAGGTGCCCATCATGGAAATGTCGTGGGGCTGTGGGCCAGTGTGCTGCAGCCCACCCGAGAACGG  
CGGAAATACGTCTCCAGTGCACGGACGGCTCTCGTGGAGAGGACTTAGAGTGGAGAGACACTTAGAGTGC  
CTCGCGTGTCCCTAAGCCCCCTGCCGCCCTGCCACCTCTCGGACTCCAGCTGTGATGGAGTTGGGACAGCC  
GTGGGACCCCTGGTATTGAGCATGAAGGAATGAAGCTGGAGAGGAAGGTAAGAAGAAGAATATTAAGTA  
TATTGTAAAATAACAAAAATAGAACCTAAAAA

292/615

**FIGURE 290**

MAPGWAGVGAARVRLALALALASVLGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRNEAERLDLDRNNITR  
ITKMDFAGLKNLRVLHEDNQVSVERGAFQDLKQLERLRLNKNLQVLPPELLFQSTPKLRLDLSENQIQGIPR  
KAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEILTNNNNNISRILVTSFNHMPKIRTLRLHSNHYCDCHLAW  
LSDWLRQRRTVGQFTLCMAPVHLRGFNADVQKKEYVCAPHSSEPPSCNANSISCPSPCTCSNNIVDCRGKGLME  
IPANLPEGIVEIRLEQNSIKAIIPAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAKGLF  
DGLVSLQQLLNANKINCRVNNTFQDLQNINLLSILYDNKLQTIISKGLFAPLQSITQLHLAQNPVFCDCHLKWLA  
YLQDNPIETSGARCSSPRLANKRISQIKSKKFRCSGSDEYRSRFSSECFMIDLVCPEKRCCEGTIVDCSNQKLVR  
IPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPNLRKINLSNNNIKEVREGAFDGAASVQEIMLTGNQLETVHGRV  
FRGLSGLKTLMRLRSNLISCVSNTFAGLSSVRLLSLYDNRITTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLG  
KWLRKRRIIVSGNPRCQKPFKLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGRLALPRGM  
PKDVTELYLEGNHLTAVPRELSALRHLLIDLSNNNSISMLNTFSNMSHLSTLILSYNRIRCIPVHAFNGLRLS  
RVLTIHGNDISSLVPEGSFNDLTSLSHLALGTNPLHCDCSLRWLSEWVKAGYKEPGIARCSSPEPMADRLLLTTPT  
HRFQCKGPVDINIVAKCNACLSSPCKNNNGTCTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDS  
HKDGFSCSCPCLGFEGQRCEINPDCCEDNDCEENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLCQHEAK  
CIPLDKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTCCTCPQGFSGPFCEHPPPMVLLQTSPCDQ  
YECONGAQCIVVQQEPTCRCPGFGAGPRCEKLITVNFVGKDSYVELASAKVRPQANISLQVATDKDNGILLYKGD  
NDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHSVELTLNQTLNLVVDKGTPKSLGKLQKQPAVGINS  
PLYLGGIPTSTGLSALRQGTDRPLGGFHGCIEVRRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDS  
VVCECRPGWTGPLCDQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKNDSANACSAFKCHHGQCHIS  
DQGEPYCILCQPGFSGEHCQQENPCLGQVVRREVIRRQGYASCATASKVPIMECRGGCGPQCCQPTRSKRRKYVFQ  
CTDGSSFVEEVERHLECGCLACS

**Signal peptide:**  
amino acids 1-27

293/615

FIGURE 291

GGATGCAGGACGCTCCCTGAGCTGCCTGTACCGACTAGGTGGAGCAGTGTTCAGGCTTCCGCAGACTCAACTGAGA  
AGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTCAGTTCTGTCTCCGGCAGGCTTGAGGATGAAGGCTG  
CGGGCATTCTGACCCTCATGGCTGCCTGGTACAGGCGCCGAGTCAAATCTACACTCGTTGCAAACGGCAA  
AAATACTCGAGGGCTGGCTGGACAATTACTGGGCTTCAGCCTGGAAACTGGATCTGCATGGCATATTATG  
AGAGCGGCATACAACACACAGCCCCGACGGCTGGATGACGGCAGCAGTCAACAGCTGGCATCTTCCAGATCAACA  
GCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAAACCAACTGCCATGTCGCTGCTCAGCCTTGATCACTG  
ATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGAGACACAAGGAATGAACATTGGCAAGGCT  
GGAAGAAAACATTGTGAGGGCAGAGACCTGTCCGAGTGGAAAAAGGCTGTGAGGTTTCCTAAACTGGAACGGAC  
CCAGGATGCTTGCAGCAACGCCCTAGGATTGCAGTGAATGTCCAATGCCTGTGTCATCTGTCCCCTTCC  
CCCAATATTCTCAAACCTGGAGAGGGAAAATTAGCTATACTTTAAGAAAATAATTCCATTAAATGTC

294/615

**FIGURE 292**

MKAAGILTLIGCLVTGAESKIKYTRCKLAKIFSRAGLDNWGFSLGNWICMAYYESGYNTTAPTVLDDGSIDYGIF  
QINSFAWCRRGKLKENNHCHVACSLITDDLTDAAIICARKIVKETQGMNYWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**  
amino acids 1-19

295/615

FIGURE 293

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTGTACCCAAGGAAAG  
TGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCTGCTGTTCTCATAGCGACCACCAGAGGA  
TGGAGTACAGATGAGGCTAATACTTACTTCAGGAATGGACCTGTTCTCGTCTCCATCTGCCAGAACGCTGC  
AAGGAAATCAAAGACGAATGTCTAGTGCATTGATGCCGTATTCTCCGCACTGAGAATGGTGTATCTAC  
CAGACCTCTGTGACATGACCTCTGGGGTGGCGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATGCGT  
GGGAAGTGACGGTGGCGATCGTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAAC  
TGGGCAACTACAACACCTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCCTGGCTACTACGAC  
ATCCAGGCCAAGGACCTGGCATCTGCCACGTGCCAATAAGTCCCCATGCAGCACTGGAGAACAGCTCCCTG  
CTGAGGTACCGCACGGACACTGGCTCCTCAGACACTGGACATAATCTGTTGGCATCTACCAGAAATATCCA  
GTGAAATATGGAGAAGGAAAGTGGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTGGCGACGCC  
CAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGAATTCACTGCGGGATTGTTCAAGGGTATT  
AATAACGAGAGAGCAGCCAACGCCCTTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATT  
GGTGGAGGGAGGAGATACTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTCTGGTTTGATTGGAGTGGATAT  
GGAACCTATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTCTATTCTATCGTTGAGGTTT  
TGTGGGAGGGAACCCAGACCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAAACTACCCAGTAGCTAGA  
ATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAA

296/615

**FIGURE 294**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVIYQTFCDMTSG  
GGGWTLVASVHENDMRGKCTVGRWSSQQGSKADYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWH  
HVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYGECKCWTDNGPVI  
YGQREFTAGFVQFRVFNNERAANALCAGMVRTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSS  
REITEAAVLLFYR.

297/615

**FIGURE 295**

CAGGCCATTGCATCCCACTGTCCTGTGTCGGAGCCAGGCCACACCGTCTCAGCAGTGTCAATGTGTTAAAAA  
CGCCAAGCTGAATATATCATGCCCTATTAAAACCTGTACATGGCTCCCCATTGGTTTGGAGAAAGTTCAAG  
CTTTTACCTGGTGTGCCTGTATCCCAGTGTTCAGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGT  
CACTTCCCAGATCTGCTCTCACCAAGAGAGATTCTTCTTAAACGACTATAACAGGGCCCAATTGACTGGATA  
GAGGAATACACCACAGGCATGGCAGACTGTCATCTTAGTCACAGCAGTTCACAGCTGCTGTTTAAGGAAACA  
TTCAAGTCCCTGTCACATAGACCTGATGTCCTCTATCCATCTCAAATGTCACCAGCTTGACTCAGTTGTT  
CCTGAAAAGCTGGATGACCTAGTCCCCAAGGGAAAAAATTCTGCTGCTCTCATCAACAGATAAGAAAG  
AAAAATCTGACTTTGGCACTGGAAGCCCTAGTACAGCTGCGTGGAGATTGACATCCAAAGATTGGAGAGGGTT  
CATCTGATCGTGGCAGGTGGTTATGACGAGAGACTGCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATG  
GTCCAACAGTCCGACCTTGGCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCCCTCCTC  
CACAGCTGCACGTGTGCTTACACCCAAGCAATGAGCACTTGGCATTGTCCTCTGGAGCCATGTACATG  
CAGTGCCAGTCATTGCTGTTAATTGGGTGGACCCCTGGAGTCCATTGACCAAGTGTACAGGGTTCTGTGT  
GAGCCTGACCGGGTGCACCTCTCAAGCAATAGAAAAGTTCATCGTGAACCTTCTTAAAGCCACCATGGC  
CTGGCTGGAAGAGCCAGAGTGAAGAAAATTCCCTGAGCATTACAGAACAGCTCTACCGATATGTTACC  
AAACTGCTGGTATAATCAGATTGTTTAAGATCTCCATTAAATGTCATTTTATGGATTGTAGACCCAGTTG  
AACCAAAAAGAAAACCTAGAATCTAGCAAGAGAGATCTTAAAAAAATAACTGAGTCTTGAATGTGAGCCA  
CTTCCCTATATACACACCTCCGTCCACCTTTCAGAAAAACATGTCATTGCTATATCATTCCAATTT  
TGCCAGTGTAAAGTACAAATGTGGTGTCACTTCATGTCAGCAGAGTATTTAATTATATTCTGGGATTAT  
TGCTCTCTGTCTATAAAATTGAAATGATACTGTGCCTTAATTGGTTTCATAGTTAACGTGTATCATTATCA  
AAGTTGATTAATTGGCTTCATAGTATAATGAGAGCAGGGCTATTGAGTTCCAGATTCAATCCACCGAAGTGT  
TCACTGTCATCTGTTAGGAATTGGTGTCTGTCTGGATCCATAGCGAGAGTGTCTGTATTTTT  
TTAAGATAATTGTATTTGCACACTGAGATATAATAAAAGGTGTTATCATAAAAAAAAAAAAAA

298/615

FIGURE 296

MPLLKLVHGSPLVFGEKFKLFTLVSACIPVFRLLARRKKILFYCHFPDLLLTKRDSFLKRILYRAPIDWIEEYTTG  
MADCILVNSQFTAASFKETFKSLSHIDPDVLYPQLNVTSFDSVVPEKLDLVPKGKKFLLLSINRYERKKNLTLA  
LEALVQLRGRRLTSQDWERVHLIVAGGYDERVLENVEHYQELKKMVQQSDLGQYVTFLRSFSQDKQKISLLHSCTCV  
LYTPSNEHFGIVPLEAMYMQCPVIAVNSGGPLESIDHSVTGFLCEPDGVHFSEAIKFIRESLKATMGLAGRAR  
VKEKFSPEAFTEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

299 / 615

FIGURE 297

GAATACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCAATGTTGGACTTCGCGATCTCGCGTACCTTC  
TTGCTGGCGTTGGTGGGAGCCGTGCTCACCTCTATCCGGCTTCCAGACAAGCTGCAGGAATTCCAGGGATTACT  
CCAACATGAAGAAAAAGATGGTAATCTTCAGATATTGTGAATAGTGGAAAGTTGCATGAGTCCTGGTTAATTG  
CATGAGAGATATGGGCCTGTGGCTCCTCTGGTTGGCAGGCGCCTCGTGGTAGTTGGGACTGTTGATGTA  
CTGAAGCAGCATATCAATCCAATAAGACATCGGACCCTTTGAAACCAGTGAAGTCATTAAAGGTATCAA  
TCTGGTGGTGGCAGTGTGAGTAAAACCACATGAGGAAAAATTGTATGAAATGGTGTGACTGATTCTCTGAAG  
AGTAACCTTGCCCTCCTCTAAAGCTTCAGAAGAATTATTAGATAAATGGCTCCTACCCAGAGACCAGCAC  
GTGCCCTCAGCCAGCATATGCTGGTTGCTATGAAGTCTGTTACACAGATGGAATGGTAGTACATTGAA  
GATGATCAGGAAGTCATTGCTCCAGAAGAACATGGCACAGTTGGCTGAGATTGGAAAAGGCTTCTAGAT  
GGGTCACCTGATAAAAACATGACTCGGAAAAACAATATGAAGAATGCCCTCATGCAACTGGAGTCTGTTTAAGG  
AACATCATAAAAAGAACGAAAAGGAAGGAACCTCAGTCAGTCAACATATTTCATTGACTCCTTAAG  
AATGACCAACAGATCTAGAAGACAGTATGATATTTCTGGCCAGTTGCATAAAACTGCAAATTGTGTACC  
TGGGCAATCTGTTTTAACCACCTCTGAAGAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTTGGA  
AATGGTCTGTTACTCCAGAGAAAATTGAGCAGCTCAGATATTGTCAAGCATGTGCTTGTGAAACTGTTGAACT  
GCCAAACTGACTCCAGTTCTGCCAGCTCAAGATATTGAAGGAAAATTGACCGATTATTATTCCCTAGAGAG  
ACCCTCGTCTTTATGCCCTGGTGTGGTACTTCAGGATCTAAACTTGGCATCTCACACAAGTTGATCCA  
GATCGGTTGATGATGAATTAGTAATGAAAATTGTTCTCACTGGATTCTCAGGCACACAGGAGTGTCCAGAG  
TTGAGGTTGATATATGGTACCAAGTACTCTTAGTGTATTGGTAGAGAGACTGCACCTACTTCTGTGGAG  
GGACAGGTTATTGAAACAAAGTATGAACCTGGTAACATCATCAAGGGAAGAAGCTGGATCACTGTCTAAAGAGA  
TATTAAAATTATACATTAAACCAACTTAAATTGATTGAGGAAAACAACCATTAAAAAAATCTATGTTG  
AATCCTTTATAAACCAACTTAAACCAACTTAAACACCTATTGACTTAA

300/615

**FIGURE 298**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAIGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVSFWFGR  
RLVVSLGTVDVLKQHINPNKTSDPFETMLKSLLRYQSGGGSVSENHMRKKLYENGVTDSILKSNFALLKLSEELL  
DKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFEDDQEVRFQKNHGTWSEIGKGFLDGSLDKNMTRKKQYE  
DALMQLESVLRNIIKERKGRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSEEVQK  
KLYEEINQVFGNGPVTPEKIEQLRYCQHVLCETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP  
NTWPSPHKFDPDRFDELVMKTSSLGFSGTQECPELRFAYMVTIVLLSVLVKRLHLLSVEGQVIETKYELVTSS  
REEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

301/615

FIGURE 299

CTAGATTGTCGGCTGCAGGGAGACTTCAGGAGTCGCTGTCTGAACCCAGCCTCAGAGACC GCCGCCCTT  
GTCCCCGAGGGCCTAGGCCGGGCTCAGGGCTTGTGCCCTCGCTCCTGACGCTCCTGGCGCATCTGGTGGT  
CGTCATCACCTTATTCTGGTCCCAGGACAGCAACATAACAGGCCTGCCTGCCTCACGTTCACCCCCGAGGAGTA  
TGACAAGCAGGACATTCACTGGTGGCCGCCTCTGTCAACCTGGCCTCTTGAGTGGAGCTGGCCGGTT  
CCTCTCAGGAGTCTCCATGTTAACAGCACCCAGAGCCTCATCTCCATTGGGCTCACTGTAGTGCATCCGTGGC  
CCTGTCCTCTTCATATTGAGCGTTGGGAGTGCACTAACGTATTGGTACATTTGTCTTGAGTGCAGTGCCTTCC  
AGCTGTCACTGAAATGGCTTATTGTCACCGTCTTGGCCTGAAAAAGAAACCTTCTGATTACCTTCATGACG  
GGAACCTAAGGACGAAGCCTACAGGGCAAGGGCCGCTCGTATTCTGGAAGAAGGAAGGCATAGGCTTCGGTT  
TTCCCTCGGAAACTGCTCTGCTGGAGGATATGTGTTGGAATAATTACGTCTGAGTCTGGGATTATCCGCATT  
GTATTTAGTGTGTTGTAATAAAAATGTTTAGTAACATTAAGACTTATACAGTTTAGGGACAATTAAA  
AAAAAAAAAA

302/615

**FIGURE 300**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFAVELAGFLSGV  
SMFNSTQSLISIGAHCSASVALSFIFERWECTTYWYIFVFCSALPAVTEMALFVTVFGLKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

303 / 615

FIGURE 301

CTGGGACCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAAGAATGCAACTGACTCGCTGCTGC  
TTCGTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGCCAGGATGATGGTCCTCCGGCTCAGAGGAC  
CCTGAGCGTGTGACCACAGAGGGCCAGCCCCGGCCGGCTCGGAAGCGGGCACATCTCACCTAAGTCC  
CGCCCCATGCCAATCCACTCTCCTAGGGCTGCTGGCCCCGCTGGGGAGGCTGGGGATTCTGGCAGGCC  
CCCAACCGCCCAGACCACAGCCCCCACCTCAGCCAAGGTGAAGAAAATCTTGCTGGCGACTTCTACTCC  
AACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAAGATTGTTGGACCATGGCAATGGGACCTTCAGCCTC  
CACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTCCCCCAGTAAAGCTGTAGAGTTC  
CACCAAGGAAACAGCAGATCTTCATCGAAGCCAAGGCCCTCCAAAATCTCAACTGCCGATGGAGTGGAGAAGGTA  
GAACGGGGCCCGGCCGGACCTCGCTTGACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCA  
GCCACCTGGAGCTGCTCCCAGCCCTCAAAGTCGTCTGTCTACATCGCCTCTACAGCACGGACTATCGGCTG  
GTCCAGAAGGTGTGCCAGATTACAACATACCATAGTGATAACCCCTACTACCCATCTGGGTAACCCGGGCAGGC  
CACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCCTGCCATGCAGGAGACCATCTGGACACCCGGCAGGGAAAGGG  
GTTGGGCCTCAGGCAGGGAGGGGGTGGAGACGAGGAGATGCCAAGTGGGCCAGGGCAAGTCTCAAGTGGCAG  
AGAAAAGGGTCCCAAGTGCTGGTCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTG  
GGCTCTCTGTGCAGCCTCACAGGGCTTGCCACGGGCCACAGAGAGATGCTGGGTCCCCGAGGCCTGTGGCAG  
GCCGATCAGTGTGGCCCCAGATCAAGTCATGGAGGAAGCTAACGCCCTGGTTCTGCCATCCTGAGGAAAGATA  
GCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTGTCAACTTAGGATGGCTGAGAGGGCTTCCTAG  
GAGCCAGTCAGCAGGGTGGGTGGGCCAGAGGAGCTCCAGCCCTGCCAGTGGCGCCCTGAGCCCCTGTC  
GTGTGCTGAGCATGGCATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTCTGACAGATTGACCATCTGTCT  
CCAGCCAGGCCACCCCTTCCAAAATTCCCTCTGCCAGTACTCCCCCTGTACCAACCCATTGCTGATGGCACA  
CCCATCCTTAAGCTAACAGACAGGAGATTGTGGCCTCCCACACTAACGCCACAGCCCATTCCGCGTGTGTC  
CCTCTCCACCCCAACCCCTGCTGGCTCCTCTGGAGCATCCATGCCCGAGAGGGGCTCAACAGTCAGCC  
TCACCTGTCAGACCGGGGTTCTCCGGATCTGGATGGCCGCCCTCTCAGCAGGGGAGGGGTGGGTGGGGGGAGGG  
CGGGCCGCAGAGCATGTGCTGGATCTGTTCTGTGTCTGTGGGTGGGGGGAGGGGAGGGAAAGTCTTGTGA  
AACCGCTGATTGCTGACTTTGTGTGAAGAATCGTGTCTGGAGCAGGAAATAAGCTTGCCCCGGGGCA

304/615

**FIGURE 302**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLAPPGEA
WGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVP
PSKAVEFHQQQIFIEAKASKIFNCRMEEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPKVVVCYIAF
YSTDYRLVQKVCPDNYHSDTPYYPSG
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

305/615

**FIGURE 303**

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCCTCGGGCTGCGCTGCCCTTATGTCT  
TCACCATGCCATCGAGCCGTTGCGTATCATCTCCTCATGCCGGAGCTTCTTCTGGTTGGTGTCTACTGA  
TTTGTCCCTTGTGGTCATGGAAGAGTCATTATTGACAACAAAGATGGACCAACACAGAAATATCTGCTGA  
TCTTGAGCGTTGTCTGTCTATATCCAAGAAATGTCGATTCGATATTATAAACTCTAAAAAAGCCA  
GTGAAGGTTGAAGAGTATAAACCCAGGTGAGACAGCACCCCTATGCCACTGCTGGCTATGTTCTGGCTTGG  
GCTTGGAAATCATGAGTGGAGTATTTCTTGTGAATACCCTATCTGACTCCTGGGCCAGGCACAGTGGCA  
TTCATGGAGATTCTCCTCAATTCTCCTTATTCAGCTTCATGACGCTGGCATTATCTGCTGCATGTATTCT  
GGGCATTGTATTTTGATGGCTGTGAGAAGAAAAGTGGGCATCCTCCTATCGTTCTCCTGACCCACCTGC  
TGGTGTCAGCCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTCA  
TGGGCACCTGGCATTCTAGCTGCCGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTGCCAAGACAAGA  
ACTTCTTCTTACAACCAGCGCTCCAGAACCTCAGGGAACCGACACTCCAAACCGCAGACTACATCTTA  
GAGGAAGCACAACTGTGCCTTTCTGAAAATCCCTTTCTGGTGGATTGAGAAAGAAATAAAACTATGCAGATA

306/615

**FIGURE 304**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSSLISLIVWFMARVIIDNKDGPTQKYLLIFG
AFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGP GTVGIHG
DSPQFFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGT
WAFLAAGGSCRSLKLCLLCQDKNFLYNQRSR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

307/615

**FIGURE 305**

308/615

**FIGURE 306**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM  
LTLPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLIHSIFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

309/615

**FIGURE 307**

CCGGGGACATGAGGTGGATACTGTCATTGGGCCCTTATTGGGTCCAGCATCTGTGGCCAAGAAAATTTTG  
GGGACCAAGTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAAATTGAGTCAACTAGTGAATTCAAACA  
ACTTGAAGCTCAATTCTGAAATCTCCCTCCTCAATCGGCCGTGGATGTCCTGGTCCCCTGTCAGTC  
TCGAGGCATTTAAATCTTCCCTGAGATCCCAGGGCTTAGAGTCAGCAACTGAGAATTGAGGACCTGCAGGGCCCTT  
TAGACAATGAAGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTCAACTACGGGGCTT  
ACCATTCCCTGGAAGCTATTACACAGAGATGGACAACATTGCCGAGACTTCTGACCTGGCAGGGAGGCTGA  
AGATTGGACATTGTTGAAAACCGGCCGATGTATGACTGAAAGTCAGCACTGGGAAAGGCGTGAGGCCGG  
CCGTTGGCTGAATGCAGGCATCCATTCCCAGAGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGA  
TTGTATCTGATTACCAAGAGGGATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTCTTGTGCTGTGG  
CCAATCCTGATGGATATGTGTATACTCAAACCTAAAACCGATTATGGAGGAAGACGCGGTCCGAAATCTGGAA  
GCTCCTGCATTGGTGTGACCCAAATAGAAACTGGAACGCTAGTTTGCAAGGAAAGGGAGCCAGCGACAACCCCT  
GCTCCGAAGTGTACCATGGACCCACGCCAATTGGAAGTGGAGGTGAAATCAGTGGTAGATTTCATCCAAAAC  
ATGGGAATTCAAGGGCTCATGCACCTGCACAGCTACTCGCAGCTGATGTATCCATATGGGTACTCAGTCA  
AAAAGGCCAGATGCCAGGAACTCGACAAGGTGGCGAGGCTGCGGCCAAAGCTCTGGCTTCTGTCGGGCA  
CTGAGTACCAAGTGGTCCCCACCTGCACACTGTCTATCCAGCTAGCGGGAGCAGCAGCTGGCGTATGACA  
ACGGCATCAAATTGCAATTGAGTTGAGAGATAACGGGACCTATGGCTTCCCTGCCAGCTAACCCAGA  
TCATCCCCACTGCAGAGGAGACGTTGGCTGGGACATGAGGAGCTGGGGACAAACCTCTACT**TAGG**  
CGATGGCTCTGCTCTGCTACATTATTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTT  
CCTACCTGTGTGAGTCAGAGCCCTCTGGGTTGTGGAGCACACAGGCCCTGCCAGCTCCAGGCTCCGGAG  
TCGTGTGTCTGGGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTGGTCTGCTGTTTGATG  
AGCCTTTGTCTGTTCTCCTCCACCCCTGCTGGCTGGCGCTGCACTCAGCATCACCCCTCCTGGTGGCAT  
GTCTCTCTACCTCATTAGAACCAAAGAACATCTGAGATGATTCTACCCCTCATCCACATCTAGCCAAGC  
CAGTGCACCTTGCTCTGGCACTGTGGGAGACACCAACTGTCTTAGGTGGCTCAAAGATGATGAGAATT  
CCTTAATTCTCGCAGTCCTGGAAAATATTTCCTTGAGCAGCAAATCTGTAGGGATATCAGTGAAGGT  
CTCTCCCTCCCTCCTCTGTTTTTTTGAGACAGAGTTGCTCTGTTGCCAGGCTGGAGTGTGA  
TGGCTCGATCTGGCTCACCACAACCTGCCCCGGGTTCAAGCAATTCTCTGCCCTAGCCCTTGAGTAGC  
TTGGTTTATAGGCGCATGCCACCATGCGCTTAATTGTGTTTTAGTAGAGACAGGGTTCTCCATGTTGGT  
CAGGCTGGCTCAAACCTCCACCTCAGGTGATCTGCCCTCCCTGGCCTCCAGAGTGTGGGATTACAGGTGTG  
AGCCACTGTGCCGGGGCCGCTCCCTCTTTAGGCCCTGAATACAAAGTAGAAGATCACTTCCCTCAGTGTG  
TGAGAACATTCTAGATACTACAGTTCTACTCCCTCTTGTGTTATTCAAGTGTGACCCAGGATGGCGGGAGGG  
GATCTGTGCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAAGTGACCATCTAAATTGAGGATGGTGAATT  
ATCCCCATCTGCTTAATGGGCTTACCTCCTCTTGCCTTTGAACTCACCTCAAAGATCTAGGCCCTCATCTTAC  
AGGTCTAAATCACTCATCTGGCCCTGGATAATCTCACTGCCCTGGCACATTCCATTGTGCTGTGTTGTGTT  
GTGTTCTGCTGGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTT  
TTTGATCTGGACCACAAGTCTAAGTAGAGCAAGAATTCAACCAAGCTGCCCTTGTTGTTGTTGTTGTTGTT  
CAGCACGTACCATCTGTCCTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT  
TCTAACCTCCTGCCCTAGGATTGTACAGCATCTGGTGTGCTTATAAGCCAATAATTCAATGTGAAAAAAA  
AAAAAAAAAA

310/615

**FIGURE 308**

MRWILFIGALIGSSICQEKFFGDQVLRINVNRNGDEISKLSQLVN SNNLKLNFWKSPSSFNRPVDVLVPSVSLQA  
FKSFLRSQGLEYAVTIEDLQALLDNEDEMHQHNEGQERSNNFNYGAYHSLEAIYHEMDNIAADFPDLARRVKIG  
HSFENRPMYVLKFSTGKGVRRAVWLNAGIHSREWIQSATAIWTARKIVSDYQRDPAITSIKEKMDIFLLPVANP  
DGYVYTQTQNRLWRKTRSRRNPGSSCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDIFIQKHGN  
FKGFIDLHSYSQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVGSTEYQVGPTCTTVYPASGSSIDWAYDNGI  
KFAFTFELRDTGTYGFILLPANQIIPTAETWLGLKTIMEHVRDNL

**Signal peptide:**  
amino acids 1-16

311/615

**FIGURE 309**

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGCCTGAGTCCAAGAT  
TCTTCCCAGGAACACAACAGTAGGAGACCACGCTCTGGAAGCACCGCCTTATCTCTCACCTTCAGTCCC  
CTTCTCAAGAACATCCTCTGTTCTTGCCTCTAAAGTCTGGTACATCTAGGACCCAGGCATCTGCTTCCAGC  
CACAAAGAGACAGATGAAGATGCAGAAAGGAATGTTCTCCCTATGTTGGTCTACTATTGCTTAAAGCTGC  
AACAAATTCCAATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCAGTGGAGCCAGCACGCCAC  
CAACTCTGGTCCAGTGTGACCTCCAGTGGGATCAGCACGCCACCATCTCAGGGTCCAGCGTGCACCTCCAATGG  
GGTCAGCATAGTCACCAACTCTGAGTCCACATACAACCTCCAGTGGGATCAGCACGCCACCAACTCTGAGTCAG  
CACAGCGTCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACCTCAGTGGGAGCAGCACGCCAC  
CAACTCTGAGTCCAGCACACCCTCAGTGGGAGCAGCACGCCACCAACTCTGAGTCCAGCACAAGCTGGGAGCAGCACGCCAC  
CACACTCTCCAGTGGGAGCAGCACGCCACCAACTCTGACTCCAGCACAACCTCAGTGGGAGCAGCACGCCAC  
CAACTCTGAGTCCAGCACAAACCTCAGTGGGAGCAGCACGCCACCAACTCTGAGTCCAGCACAAGCTGGGAGCAGCACGCCAC  
GGCCAGCAGTCCAGCACACCCTCAGTGGGAGCAGCACGCCACCAACTCTGAGTCCAGCACAACCTCAGTGGGAGCAGCACGCCAC  
AACGACCTCCAATGGGCTGGCACAGCCACCAACTCTGAGTCCAGCAGCACGCCACCTCAGTGGGAGCAGCACGCCAC  
CAACTCTGACTCCAGCACAGTGTCCAGTGGGAGCAGCACGCCACCAACTCTGAGTCCAGCAGCACGCCACCTCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCAGCACGCCACCTCAGTGGGAGCAGCACGCCACCAACTCTGAGTCCAG  
CACAAACCTCAGTGGGAGCAGCACGCCACCAACTCTGAGTCCAGCAGCACGCCACCAACTCTGAGTCCAGCAGCACAGTCCAG  
CAATTCTGAGTCCAGCACACCCTCAGTGGGAGCAGCACGCCACCAACTCTGAGTCCAGTACGACCTCAGTGG  
GGCCAACACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGAGCAGCACGCCACCAACTCTGAGTCCAG  
CACAAACCTCAGTGGGAGCAGCACGCCACCAACTCTGAGTCCAGCAGCACGCCACCAACTCTGAGTCCAGTGG  
CAACTCTGACTCCAGCACAAACCTCAGTGGGAGCAGCACGCCACCAACTCTGAGTCCAGTGG  
GATCAGCACAGTCACCAATTCTGAGTCCAGCACAACCTCAGTGGGAGCAGCACGCCACCAACTCTGGGAGCAG  
TGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGAATGCACACAACCTCCATAGTCATCTACTGCAGT  
GAGTGAGGCAAAGCCTGGTGGGAGCAGCAGCTCTGAGTCCAGTGGGAGGAAATCTTCATCACCTGGTCTGGTTGTGGCGGC  
CGTGGGAGCAGCAGCTGGTGGCTCTTCTGAGTCCAGTGGGAGGAAACAGCCTGTCCTGAGAAACACCTTAACACAGCTGT  
CTACCCACCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAAATCATGGAGGCCCCCACAGGCCAG  
GTGGAGTCTAATGGTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCAGGGAGGAACAGCGGGGCC  
CTGAAGCAGCCCCGGAAAGCAAGTGCCTGCATTCTCAGGAAGGAAGAGACCTGGCACCCAAAGACCTGGTTCTCTT  
CATTCTACCCAGGAGACCCCTCCAGCTTGAGATCCTGAAATCTTGAAGAAGGTATCTCCTCACCTTCT  
TGCCTTACCAAGACACTGGAAAGAGAAATATAATTGCTCATTTAGCTAAGAAATAATACATCTCATCTAACAC  
ACACGACAAAGAGAAGCTGTGCTGCCCCGGGGTGGGTATCTAGCTCTGAGATGAACCTCAGTTAGGAGAAAAC  
CTCCATGCTGGACTCCATCTGGCATTCAAACAGTAAACCTCAAAGACCTAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

312/615

**FIGURE 310**

MKM**Q**KGNVLLMFGLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATIS  
GSSVTSNGSVI**T**NSEFHTTSSGISTATNSEFSTASSGISIATNSESSTSSGASTATNSESS  
TPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSSTS  
SGASTATNSESSTSSGASTATNSESSTVSSRASTATNSESSTSSGASTATNSESRTTSNGA  
GTATNSESSTSSGASTATNDSSTVSSGASTATNSESSTSSGASTATNSESSTSSGASTA  
TNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTSSGANTATNS  
ESSTVSSGASTATNSESSTSSGASTATNSESSTSSGASTATNDSSTTSEASTATNSESS  
TVSSGISTVTNSESSTSSGANTATNGSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGS  
LVPWEIFLITLVSVVAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPBPGGNHGAP  
HRPRWSPNWFWRPVSSIAMEMSGRNSGP

**Signal peptide:**  
amino acids 1-20

**Transmembrane domain:**  
amino acids 510-532

313/615

**FIGURE 311A**

CTAAGCCGGAGGATGTGCAGCTGGCGCGCGCAGCTACGAAGAGGACGGGACAGGCCGTGCGAACCGA  
 GCCCAGCCAGCCGGAGGACGCCGGCAGGGGGACGGGAGCCCAGCTCGTCTGCCGCCGCGTCGCCGTCG  
 CGGGCATGGTCCCCCTCTAAAGGCAGGCCGG  
 CCTGGGGGGGGCTCGGG  
 CGCGCTAGGGCGGGCTGGCCTCGTGG  
 GGCAGGG  
 TGCTCGGGCTCGTCTGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGGGCTTCGAGCTGAAGCGAGCG  
 GCCCACGGCGCCGCGCAGCCCCGAGGGCTGCCGGTCCGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGG  
 GCGATGCCGCCGGGGCGCAGCTGGCCGCCGGCTGGACCCAGATGGCGGCCGCCGACAGGAACCTTCTCT  
 TCGTGGGAGTCATGACCGCCCAGAAATACCTGCAGACTCGGGCGTGGCGCCTACAGAACATGGTCAAAGACAA  
 TTCTGGAAAGTTCAAGTCTGACACATCTGTACCAATTCCAGTAGTGTGCCACTACGGG  
 GTGTGGACGACTCCACCCGCCAGAAGAAGTCTTCATGATGCTCAAGTACATGCACGACCAACTTGGACA  
 ACTATGAATGGTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACTTCTGAGGAGTT  
 TGAACAGCAGCGAGCCCTCTTCTTGGCAGACAGGCCCTGGGACACAGGAAAGAAATGGGAAAACGGCCCTGG  
 AGCGTGGTGGAGAAACTTCTGCATGG  
 ACATGGCAAGTGTCTCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGAGGTGTGTCCGGAGGGTTG  
 CAGGGGTGCACTGTCTGGCTTATGAGATGCCAGCTTTATGAGAACATGAGGAGGGGGGGGGGGGGGGGGGG  
 ACATTAGAGATCTCCATAACAGTAAAATTACCAAGCTATCACATTACACCCAAACAAAACCCACCCCTACCAGT  
 ACAGGCTCCACAGCTACATGCTGAGCCGAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCGCGAA  
 TTGTCTGTGAGCAAATACAGCAACAGAAATTCTAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCTTCA  
 TGAGGTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTCTGACTGGAAAATACTTGTATTGGCAG  
 TTGACGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAGCCTGGACGACATTGTATGCAGGTCA  
 TGGAGATGATCAATGCCAACGCCAGACAGGAGGGCGCATCTGACTTCAAAGAGATCCAGTACGGCTACCGCC  
 GGGTGAACCCCAGTGTATGGGCTGAGTACATCTGGACCTGCTCTGTACAAAAGCACAAGGGAGAAAA  
 TGACGGTCCCTGTGAGGAGGACCGTGTATTTACAGCAGACTTCAGCAAATCCAGTTGTGGAGCATGAGGAGC  
 TGGATGCCAACAGAGTGGCCAAGAGAATCAATCAGGAATCTGGATCTTGCTCTCTCTCAAACCTCCCTGAAGA  
 AGCTCGTCCCCCTTCAGCTCCCTGGTCAAGAGTGGAGCATCAGGAAACAGGAAATTTGGGAAACTTGTGAGAAGCAGT  
 TTCTTTGTCTGGCTTCAGCATGTTGAGATTATGGGAAACTTGTGAGAACAGCTGTCTTATCCCCAAATC  
 AGAACGTCAAGCTGTTCTGCTTCAATTCTGACTCCAACCTGACAAGGGCAAACAAAGTGAACGTGATGA  
 GAGATTACCGCATTAAAGTACCCATAAGCCGACATGCAAGATTGCTGTGTGGAGAGTTCAAGAGCCCTGG  
 CCCTGGAAGTAGGATCTCCAGTTAACATGAATCTTGCTCTCTGCGACGTCGACCTCGTGTGTTACTA  
 CAGAATTCCCTCAGCGATGTCGAGCAAATACAGTTCTGGCCAACAAATATATTCCAAATCATCTCAGCCAGT  
 ATGACCCAAAGATTGTTATAGTGGAAAGTCTCCAGTACAACCATTTGCCTTACTCAGAAAATGGCTTCT  
 GGAGAAAATATGGGTTGGCATACGTGTATTATAAGGGAGATCTTGTCCGAGTGGGGGTTGATGTTCCA  
 TCCAAGGCTGGGGCTGGAGGATGTGGACCTTCAACAAGGTTGTCAGGCAGGTTGAAGACGTTAGGAGCC  
 AGGAAGTAGGAGTAGTCCACGCCACCATCTGTCTTTGTGATCCCAATCTGACCCAAACAGTACAAAATGT  
 GCTTGGGGTCCAAAGCATCGACCTATGGGTCACCCAGCAGCTGGTCAAGATGTGGCTGGAAAAAAATGATCCAA  
 GTTACAGTAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCCTAATGTCTCAGTTGCTGGGAAAGACGTTT  
 TAATTCTAATTATTGTTCAAAATTTGTGATGATCAGTTGAGGTTGAAGTCCAGTACAAGGATATAATTAC  
 AAGTGGTTCTTACATAGGACTCTTAAAGATGAGCTTCTGAAACAAGAGGTGATCAGTGTGTTGCTTGGCTTGGAA  
 CACATCTTCTGCTGAAACATTATGTAGCAGACCTGCTTAACCTTGACTGAAATGTACCTGATGAACAAAATCT  
 TTAAAAAAATGTTCTTCAAGACCCCTTGTCTCCAGTCTATGGCAGAAAACGTGAACATTCTGCAAAGTAT  
 TATTGTAACAAAACACTGTAACCTGTGAAATGTTCTGTTGTGATTGTTAACATCCACAGATTCTACCTTGT  
 GTTTGTTTTTTTACAATTGTTAAAGCCATTCTGTTCAAGTGTGAGGATAAGGAAATGTGATAATA  
 GCTGTTCTCATCTGCTTCAGGAGAGCTTCCAGAGTTGATCATTCTCTCATGGTACTCTGCTCAGCATGGC  
 CACGTAGGTTTTGTTGTTGTTGTTGTTGTTGAGACGGAGTCTCAGCTGTTACCCAGGCTGGAATG  
 CAGTGGCGCAATCTGGCTCAGTTAACCTCCACTTCCGTTCAAGCAATTCCCTGCCTTGCCTCCGAGT  
 AGCTGGGATTACAGGCACACACCACGCCAGNTAGTTTTGTATTGTTAGTAGAGACGGGTTTACCAT  
 GCAAGGCCAGCTGGCCACGTAGGTTAAAGCAAGGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTG  
 TGGTAGTCATTGGCCTAAATAGACCTGGCATTAAATTCAAGAAGGATTGGAATTCTTCTTCTGACCCCT  
 CTCTTAAAGGGAAAATATTAGTTAGAATGACAAAGATGAATTATTACAATAATCTGATGTACACAGACT  
 GAAACATACACACATACACCCATAACAAACGTTGGGGAAAAATGTATTGTTGTTGTTCTTCAATTCTGCTG  
 TGTTATGTGGGTGGAGATGGTTTCAATTACTGTTGTTTATCCTTGTATCTGAAATACCTTAA

314/615

**FIGURE 311B**

TTTATTTAATATCTGTTGTCAGAGCTCTGCCATTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG  
GAGTGTGTTAGTCTGTTTATTGCAGTAAACCGATCTCAAAGATTCCCTTGGAAACGCTTTCCCCCTCC  
TTAATTTTATATTCTTACTGTTTACTAAATATTAAAGTGTCTTGACAATTGGTGCCTCATGTGTTGGG  
GACAAAAGTGAATGAATCTGCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTGTT  
TTCATTTAGATTCAAACAGTGATAGACTTGCCTTTAACACGTCAATTGGAGGGCTGCCTATTGTAATAG  
CCTGATGCTCATTTGGAAAAATAAACCGAGTGAACAATTGGTACTTTGAACCATTTGTCTCATT  
ATTCCCTGTTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAACTAAACACGAAAAAA

315/615

**FIGURE 312**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 91812, pi: 9.52, NX(S/T): 3  
MAARGRRRAWLSVLLGLVLGFVLASRLVLPASELKAGRPRRRASPEGCRSGQAAASQAGGARG  
DARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEGSD  
TSVPIPVVPLRGVDDSYPPQQKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLRSLN  
SSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYTTTED  
VEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPPYQYRL  
HSYMLSRKISELRHRTIQLHREIVLMSKSYNTIEHKEDLQLGIPPSFMRFQPRQREEILEWEF  
LTGKYLYSAVDGQPPrRGMDAQREALDDIVMQVMEMINANAKTRGRRIIDFKEIQYGYRRVNP  
MYGAEYILDLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKRINQESGSL  
SFLSNSLKKLVPFQLPGSKSEHKEPKDKKINILIPSLSGRFDMFVRFMGNFEKTCLIPNQNVKL  
VVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQFNNESSLFFC  
DVDLVFTTEFLQRCCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFTQKTGFWRNYGF  
GITCIYKGDLVRVGGFDVSIQGWGLEVDLFNKVVQAGLKTFRSQEVGVVHVHPVFCDPNLD  
PKQYKMCLGSKASTYGSTQQIQAEMWLEKNDPSYSKSSNNNGSVRTA

**Signal peptide:**  
amino acids 1-23

316/615

FIGURE 313

GGCCGGACGCCCTCCCGTTACGGGATGAATTAAACGGCGGGTCCGCACGGAGGTTGTGACCCC  
TACGGAGCCCCAGCTTGCACCGCACCCACTCGCGTCGCGCGCGTGCCTGCTTGTCA  
GGTGGGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTCTGGGAAGCTGGCA  
ACAAATGGATGATGTGATATATGCATTCCAGGGAAAGGGAAATTGTGGTGCTTCTGAACCCAT  
GGTCAATTAAACGAGGCAGTTCTAGCTACTGCACGTACTCATAAAGCAGGACTCTAAAGCT  
TTGGAATCATGGTGTATGGAAAGGGATTTACTTATACTGACTCTGTTGGGAAGCTTT  
TTGGAAGCATTTCATGCTGAGTCCCTTTACCTTGATGTTGAAACCCATCTTGGTATC  
GCTGGATCAACAACCGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCA  
TGTTTGGTGTAAAAGTGATTATAACTGGGGATGCATTGTTCTGGAGAAAGAAGTGTCA  
TCATGAACCATCGGACAAGAACATGGACTGGATGTTCTGTGGAAATTGCCTGATGCGATATAGCT  
ACCTCAGATTGGAGAAAATTGCCTCAAAGCAGTCTCAAAGGTGTTCTGGATTGGTTGGG  
CCATGCAGGCTGCTGCCTATATCTTCATTCAAGGAAATGGAAGGATGACAAGAGCCATTG  
AAGACATGATTGATTACTTTGTGATATTCAAGAACACTCAACTCCTCATATTCCCAGAAG  
GGACTGATCTCACAGAAAACAGCAAGTCTGAAGTAATGCATTGCTGAAAAAAATGGACTTC  
AGAAAATATGAATATGTTTACATCCAAGAAACTACAGGCTTACTTTGTGGTAGACCGCTAA  
GAGAAGGTAAGAACCTTGATGCTGTCCATGATATCACTGTGGCGTATCCTCACAACATTCC  
AATCAGAGAACGACCTCCTCCAAGGAGACTTCCCAGGGAAATCCACTTTCACGTCCACCG  
ATCCAATAGACACCCTCCCCACATCCAAGGAGGACCTCAACTCTGGTGCACAAACGGTGGG  
AAGAGAAAAGAGAGAGGCTCGTCCCTCTATCAAGGGAGAAGAATTTTATTACCGGAC  
AGAGTGTATTCCACCTTGCAAGTCTGAACTCAGGGTCTTGTGGTCAAATTGCTCTATAC  
TGTATTGGACCCTGTTGCATGCTGCATGCTACTCATATATTGTACAGTCTTGTAA  
GGTATTTTATAATCACCATTGTAATCTTGTGCTGCAAGAGAGAATATTGGTGGACTGGAGA  
TCATAGAACATTGCATGTTACCGACTTTACACAAACAGCCACATTAAATTCAAAGAAAATG  
AGTAAGATTATAAGGTTGCATGTGAAAACCTAGAGCATATTGGAAATGTTCTAAACCTT  
TCTAACGCTCAGATGCATTGGCATGACTATGTCGAATATTCTTACTGCCATATTGT  
TAAAGATATTGCACTTAATTGTGGAAAATATTGCTACAAATTTTTAATCTCTGAA  
TGTAATTGATACTGTGTACATAGCAGGGAGTGTGATCGGGGTGAAATAACTGGGCCAGAATA  
TTATTAAACAATCATCAGGCTTTAAA

317/615

**FIGURE 314**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIFYFILTLFWGSFFGSIFML  
SPFLPLMVFVNPSWYRWINNRLVATWLTLVALLETMFGVKVIITGDAFVPGERSVIIMNHRTR  
MDWMFLWNCLMRYSYLRLEKICLKLASKLGVPFGFWAMQAAAYIFIHRWKDDKSHFEDMIDYF  
CDIHEPLQLLIFPEGTDLTENSRSNAFAEKNGLQKYEVVLHPRTGFTFVVDRLREGKNLD  
AVHDITVAYPHNIHQSEKHLLQGDFPREIHFHVRYPIDLPTSKEDLQLWCHKRWEKEERL  
RSFYQGEKNFYFTGQSVIPPKSELRLVLLVKKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITI  
VIFVLQERIFGGLEIEELACYRLLHKQPHLNSKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

318/615

**FIGURE 315**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCTGCCTGAGACAGCTGGCTGA  
CCTCCAAATCATCCATCCACCCCTGCTGTCACTGTTTCATAGTGTGAGATCAACCCACAGG  
AATATCC**TG**GCTTTGTGCTCATTGGTTCTCAGTTCTACGAGCTGGTGCAGGACAGTG  
GCAAGTCACTGGACCGGGCAAGTTGTCAGGCCCTGGTGGGGAGGACGCCGTGTCCTG  
CTCCCTCTTCCCTGAGACCAGTCAGAGGCTATGGAAGTGCCTCTTCAGGAATCAGTCCA  
TGCTGTGGTCCACCTCTACAGAGATGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCG  
AGGGAGAAGTGAAGTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTAAGGCTAAAAAA  
CATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTCCCAGATTACGATGAGGA  
GGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTCCCTCTATTCCATCGTGGGATA  
TGTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTCCCCCAGCCCACAGCAA  
GTGGAAAGGTCCACAAGGACAGGATTGTCAGACTCAGAGCAAATGCAGATGGTACAG  
CCTGTATGATGTGGAGATCTCATTATAGTCAGGAAAATGCTGGGAGCATATTGTGTTCCAT  
CCACCTTGCTGAGCAGACTGAGGTGGAATCCAAGGTATTGATAGGAGAGACGTTTCCA  
GCCCTCACCTGGCCCTGGCTCTATTACTCGGGTTACTCTGTTGCTGCCCTGTGTTG  
TGTATGGGATGATAATTGTTCTTCAAATCCAAGGAAAATCCAGGCGAACTGGACTG  
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGAAACACGCACTGGAGGTGACTCT  
GGATCCAGAGACGGCTCACCGAAGCTCTGCCTCTGATCTGAAAACGTAAACCCATAGAAA  
AGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCTCTCA  
GGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGACAAAATGTAGGGTGGTATGT  
GGGAGTGTGTCGGGATGACGTAGACAGGGGGAGAACAAATGTGACTTGTCTCCAAACAATGG  
GTATTGGGTCTCAGACTGACAACAGAACATTGATTTACATTCAATCCCCATTATCAG  
CCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTCCTGGACTATGAGGGTGGGACCAT  
CTCCTCTCAATACAATGACCATGCTTATACCTGCTGACATGTCAGTTGAAGG  
CTTGTGAGACCTATATCCAGCATGCGATGTATGACGAGGAAAAGGGGACTCCCATTACAT  
ATGTCCAGTGTCTGGG**TG**AACAGAGAAGACCCCTGCTAAAGGGCCCCACACCACAGACC  
CAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGCCCCAGCTCCTCTCCGGAGCCTGCGC  
ACAGAGAGTCACGCCCTCACTCTCCTTAGGGAGCTGAGGTTCTCTGCCCTGACCTGTGGAGTCAGAACCC  
GCAGCGGCACTCACAGCTCCAGATGAGGGGGATTGGCCTGACCTGTGGAGTCAGAACCC  
ATGGCTGCCCTGAAGTGGGAGCGGAATAGACTCACATTAGGTTAGTTGTGAAAACCTCCATC  
CAGCTAACGATCTTGAACAAGTCACAAACCTCCAGGCTCCTCATTGCTAGTCACGGACAGT  
GATTCCCTGCCCTCACAGGTGAAGATTAAAGAGACAAACGAATGTGAATCATGCTGAGGTTGA  
GGGCACAGTGTGCTAATGATGTGTTTATATTACATTTCACCATAAAACTCTGTT  
GCTTATTCCACATTAATTACTTTCTATACCAAATCACCATGGAATAGTTATTGAACAC  
CTGCTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTCACTGATTCTATAAGGCCAG  
CATTACCTGATACCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACACAGGTCCA  
TATCCCTCATTAACACAGACACAAAATTCTAAATAAAATTAAACAAATTAAACTAAACAAT  
ATATTAAAGATGATATATAACTACTCAGTGTGTTGTCACAAATGCAGAGTTGGTTAA  
TATTTAAATATCAACCAGTGTAAATTGACACATTAATAAGTAAAAAGAAAACCATAAAAAA  
AAAAAA

319/615

**FIGURE 316**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866  
><subunit 1 of 1, 466 aa, 1 stop  
><MW: 52279, pi: 6.16, NX(S/T): 2  
MAFVLILVLSFYELVSGQWQVTGPGKFKVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAV  
VHLYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEAT  
WELRVAAL GSLPLISIVGYVDGGIQLLC LSSGWFPQPTAKWKG PQQDLS DS RANADG YSLY  
DVEISII VQENAGS SILCSIHLAEQSHEVESKV LIGETFF QPSPW RLASILLGLL C G A L C G V V M  
GMIIVFFKSKG KIQAELD WRRKH GQ AEL RDARK H A V E V TLD PETAHPKLCVSDLKTVTHRKA P  
QE VP HSEKRFTRKS VVASQGFQAGRHYWEVDVGQNVG WYVGVC RDVDRG KNNV TLSPNNGY W  
VLRLTTEHLYFTFNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLTCQFEGLL  
RPYIQHAM YDEEKGTP IFICPV SWG

**Signal peptide:**  
amino acids 1-17

**Transmembrane domains:**  
amino acids 131-150, 235-259

320/615

**FIGURE 317**

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTCAGAGAGTCGCTCTGGCTTC  
TGGGCTTGTCTGGCTCTGTCGCTGCTGCCAAGGCCTCCTGTCCCAGGGAAAGCGGCA  
GGAGCCGCCGCGACACCTGAAGGAAAATTGGGCCGATTCCACCTATGATGCATCATCACCA  
GGCACCCCTCAGATGCCAGACTCCTGGGGCTCGTTCCAGAGGTCTCACCTGCCGAGGCATT  
TGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGTAGTGGAAAGAGGTCTGATGGG  
GCAGATTATTCCAATCTACGGTTTGGGATTTTATATATACTGTACATTCTATTAAAGGT  
AAGTAGAACATCCTAACATATTACATCAATGAAATCTAATATGGCGATAAAAATCATTGT  
CTACATTAAAACCTCTTATAGTTCAAAATTATTCAAATCCATCATCTCTTAAATCCTGC  
CTCCTCTTCAAGGTACTTAGGATAGCCATTATTCAGTTCACATAAGAATGTTACTCAA  
TGTTTAAGTGTGCCCCAAAATTACAACAAAGGCAGAACTAGGACTTGAACATGGAT  
CTTTGGTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCTGCCA

321/615

**FIGURE 318**

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGRFPMMHHHQAPSDGQTP  
GARFORSHLAEAFAKKGSGGGAGGGGSGRGLMGQIIPYGFGLFLYILFKVSRIILIIHQ

322/615

FIGURE 319

CCTTCACAGGACTCTCATTGCTGGTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAG  
GAAAAGAGTTGTTGGAACCCCTGGTTATCGGCCTCGTCATCTCATATCCCTGATTGTCCT  
GGCAGTGTGCATTGGACTCACTGTTCATTATGTGAGATATAATCAAAGAACCTACAATT  
CTATAGCACATTGTCATTACAACAGACAAACTATATGCTGAGTTGGCAGAGAGGCTTCTAA  
CAATTTCAGAAATGAGCCAGAGACTTGAATCAATGGTAAAAATGCATTTATAAATCTCC  
ATTAAGGGAAAGAATTGTCAGTCTCAGGTATCAAGTCAGTCAACAGAACGATGGAGTGT  
GGCTCATATGCTGTTGATTGAGATTCACTACTGAGGATCCTGAAACTGTAGATAAAAT  
TGTTCAACTTGTACATGAAAAGCTGCAAGATGCTGAGGACCCCTAAAGTAGATCCTCA  
CTCAGTTAAAATTAAAAAAATCAACAAGACAGAACAGACAGCTATCTAAACCATTGCTGCC  
AACACGAAGAAGTAAAACCTAGGTAGAGTCAGGATCGTTGGGGACAGAACGATAGAAGA  
GGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGAGCAACCTT  
ATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTACAACATATAAGAACCTGCCAG  
ATGGACTGCTCCTTGGAGTAACAATAAAACCTCGAAAATGAAACGGGGCTCCGGAGAAT  
AATTGTCCATGAAAATACAAACACCCATCACATGACTATGATATTCTCTGCAGAGCTTC  
TAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTGTCTCCCTGATGCATCCTATGAGTT  
TCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAAATGATGGTTACAGTC  
AAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACCTCAAGC  
TTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTAGAAGGAAAACAGATGC  
ATGCCAGGGTGAECTGGAGGACCACGGTTAGTTCAAGTGCTAGAGATATCTGGTACCTTGC  
TGGAAATAGTGAGCTGGGAGATGAATGTGCGAACACCAACAAGCCTGGTGTATTA  
TACGGCCTGCAGGACTGGATTACTCAGGATCTTAAAGAGACAAAGCCTCATGGAA  
CAGATAACATTGTTGTTGGGTGTGGAGGCCATTAGAGATAACAGAATTGGAGA  
AGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAACTGTTGCTTGATGCATGTATTT  
CTTCCCAGCTCTGTCGCACGTAAGCATCCTGCTTCTGCCAGATCAACTCTGTCATCTGTGA  
GCAATAGTTGAAACTTATGTACATAGAGAAATAGATAACATTACATTACAGCCTGTA  
TTCATTGTTCTCTAGAAGTTGTCAGAATTGACTTGTGACATAATTGTAATGCATA  
TATACAATTGAAAGCACTCCTTCTCAGTTCCCTCAGCTCCTCTCATTTCAGCAAATATCCA  
TTTCAAGGTGCAGAACAGGAGTGAAAGAAAATAAGAAGAAAAATCCCTACATT  
TTGGCACAGAAAAGTATTAGGTGTTCTTAGTGGAAATTAGAAATGATCATATT  
GAAAGGTCAAGCAAAGACAGCAGAAATACCAATCACTTCATCATTAGGAAGTATGGGAAC  
GTTAAGGAAGTCCAGAAAGAACGCAAGATATTCCTTATTTCAATTCAAACAACTACTATG  
ATAAAATGTGAAGAAGATTCTGTTTTGTGACCTATAATAATTACAAACTTCATGCAATG  
TACTTGTTCTAAGCAAATTAAAGCAAATTAAACATTGTTACTGAGGATGTCAACATA  
TAACAATAAAATATAAATCACCCA

323/615

**FIGURE 320**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTDK
LYAEFGREASNNFTEMSQRLESMVKNAYKSPLREFVKSQVIKFQQKHGVLAHMLLICRFH
STEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQS
LRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIK
PSKMKRGLRRRIIVHEKYKHPHDYDISLAELSSPVYTNAVHRVCLPDASYEFQPGDVMFVTG
FGALKNDGYSQNHLRQAQVTLLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGPLV
SSDARDIWYLAGIVSWGDECAPNKPGVYTRVTALRDWITSKTGI
```

**Transmembrane domain:**

amino acids 21-40 (type II)

324/615

**FIGURE 321**

CCGGGCTCCTGGGTGAGGCCGGCAAGTTGGAGCGTGGTCAGACAATAGGGCGTGGCTACGG  
CTCGCGGAGCGCAACCAACGCTCTAGACCAGACCTGGGCTCGAGACCATAACTGTTGGCTTT  
AACAGTACGTGGCGGGCCGGAATCCGGAGTCCGGTGACCCGGGCTGTGGTCTAGCATAAAGG  
CGGAGCCCAGAAGAAGGGGCGGGGTATGGGAGAAGCCTCCCCACCTGCCCGCAAGGCGGCA  
TCTGCTGGCCTGCTGCTGCTCCTCTACCCCTGGTATCCCCTCCGCTGCAGCTCCTATCCA  
TGATGCTGACGCCAAGAGAGCTCCTGGTCTCACAGGCTCCAGAGCCTACTCCAAGGCTT  
CAGCCGACITTCCTGAAAGTAACCTGCTTCGGGCATAGACAGCTTATTCTCTGCCCAT  
GGACTTCCGGGCCTCCCTGGAACTACCACAAAGAGGAGAACCAAGGAGCAGCTGGGAA  
CAACACCCCTCTCCAGCCACCTCCAGATCGACAAGATGACCGACAACAAGACAGAGGAGGGTGC  
GATCTCCGAGAATGTGGTGGCATCCATTCAACCAGCGGAGGGAGCTCGAGGGTGATTGAA  
GGTACCCAGGATGGAGGAGAAGGAGGCCCTGGTACCCATCCAGAAGGCCACGGACAGCTCCAC  
ACAGAACTCCATCCCCGGGTGGCCTCTGGATCATTAAGCTGCCACGGCGGAGGTCCCACCAG  
GATGCCCTGGAGGGCGGCCACTGGCTCAGCGAGAAGCGACACCGCCTGCAGGCCATCCGGAT  
GGACTCCGCAAGGGGACCCACAAGGACGTCTAGAAGAGGGACCGAGAGCTCCTCCACTCC  
AGGCTGTCCCCCGAAAGACCCACTTACTGTACATCCTCAGGCCCTCTGGCAGCTGTAGGG  
TGGGGACCGGGGAGCACCTGCCTGTAGCCCCATCAGACCCTGCCCAAGCACCATAATGGAAA  
TAAAGTTCTTCTTACATCTAAAAA

325/615

**FIGURE 322**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68879
><subunit 1 of 1, 242 aa, 1 stop
><MW: 27007, pI: 8.68, NX(S/T): 2
MGEASPPAPARRHLLVLLLLLSTLVIPSAAPIHDADAQESSLGLTGLQSLLQGFSRLFL
KGNLLRGIDSLFSAAPMDFRGLPGNYHEENQEHLGNNTLSHLQIDKMTDNKTGEVLIS
ENVVASIQPAEGSFEGDLKVPRMEEKEALVPIQKATDSFHTELHPRVAFWIILPRRRSH
QDALEGGHWLSEKRHRLQAIRDGLRKGTHKDVLVEGTTESSSHSRLSPRKTHLLYILRPSR
QL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-30

**N-glycosylation sites:**

Amino acids 97-101;112-116

**N-myristoylation sites:**

Amino acids 80-86;132-138;203-209;216-222

326/615

**FIGURE 323**

AGAGAAAGAACGCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCCGAAGAACGTTCCC  
TGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCAGGGCGTGGGCACCGGGCC  
CAGCGCCGACGATCGCTGCCGTTGCCCTGGGAGTAGGATGTGGTCAAAGGATGGGCCTTC  
TCCCTACGGGCTACAATGCCAGAGAAGATCCGTGAAGTGTCTGCGCTGCCTGCTCTAC  
GCCCTCAATCTGCTCTTGTTAATGTCCATCAGTGTGGCAGTTCTGCTGGATGAGG  
GACTACCTAAATAATGTTCTCACTTTAACGTGAGAACGAGGGTAGAGGAAGCAGTCATTG  
ACTTACTTCCCTGGTTCATCCGGTCACTGATTGCTGTTGCTGTTCTTATCATTGTTGGG  
ATGTTAGGATATTGAGAACGGTAAAAGAAATCTGTTGCTTCTGCATGGTACTTGGAAAGT  
TTGCTGTCATTTCTGTGAGAACGGCTGTGGCAGTGGACATATGAACAGGAACCTATG  
GTTCCAGTACAATGGTCAGATATGGTCACTTGAAGGCCAGGATGACAAATTATGGATACCT  
AGATATCGGTGGCTACTCATGCTGGAATTTTTCAGAGAGAGTTAACGTGCTGTGGAGTA  
GTATATTCACTGACTGGTTGAAATGACAGAGATGGACTGGCCCCAGATTCTGCTGTGTT  
AGAGAATTCCAGGATGTTCAAACAGGCCACCAGGAAGATCTCAGTGACCTTATCAAGAG  
GGTGTGGGAAGAAAATGTTACCTTTGAGAGGAACCAAACACTGCAGGTGCTGAGGTTT  
CTGGGAATCTCCATTGGGTGACACAAATCCTGCCATGATTCTCACCAATTACTCTGCTCTGG  
GCTCTGTATTATGATAGAAGGGAGCCTGGACAGACCAATGATGTCCTGAAGAATGACAAC  
TCTCAGCACCTGTCATGCCCCCAGTAGAACACTGTTGAACCAAGCCTGTCAGAACATCTTGAA  
CACACATCCATGGCAAACAGCTTAATACACACTTGAGATGGAGGAGTTTAAAAAGAAATG  
TCACAGAAGAAAACCACAAACTGTTTATTGGACTTGTGAATTGGAGTACATACTATGTG  
TTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAATAACACCTAACGATATACTATTCTA  
TGCTTAAATGAGGATGGAAAAGTTCATGTCATAAGTCACCACCTGGACAATAATTGATGC  
CCTTAAATGCTGAAGACAGATGTCATACCCACTGTGAGCCTGTATGACTTTACTGAAC  
ACAGTTATGTTTGAGGCAGCATGGTTGATTAGCATTCCGCATCCATGCAAACGAGTCACA  
TATGGTGGACTGGAGCCATAGTAAAGGTTGATTACTTCTACCAACTAGTATATAAAGTACT  
AATTAAATGCTAACATAGGAAGTTAGAAAATCTAACATTGACTACGCGATCTATT  
TTCTGATGCTAAATAATTATATCAGAAAATTCATATTGGTACTACCTAAATGTGAT  
TTTGCTGGTTACTAAATATTCTACCACTTAAAGAGCAAGCTAACACATGTCCTAACG  
GATCAGGGATTGTTGATATAAGTCTGTTAAATCTGTATAATTCACTGATTTCACT  
GATAATGTTAAGAATAACCATTATGAAAAGAAAATTGCTCTGTATAGCATCATTATTTTA  
GCCTTCCTGTTAATAAGCTTACTATTCTGCTCTGGCTTATATTACACATATAACTGTTA  
TTAAATACCTAACACTAATTGAAAATTACCAAGTGTGATACATAGGAATCATTATTCA  
ATGTTAGTCTGGCTTTAGGAAGTTAAATAAGAAAATTGCACATAACTTAGTTGATTCA  
AGGACTTGTATGCTGTTTCTCCAAATGAAGACTCTTTGACACTAAACACTTTAAAAA  
AGCTTATCTTGCCTCTCCAAACAAAGCAATAGTCTCAAGTCATATAAATTCTACAGA  
AAATAGTGTCTTTCTCCAGAAAATGCTGTGAGAATCATTAAACATGTGACAATTAG  
AGATTCTTGTGTTATTCACTGATTAATATACTGTGGCAAATTACACAGATTATAAATT  
TTTACAAGAGTATAGTATATTATTGAAAATTGGAAAAGTGCATTTACTGTATTGTTGAT  
TTGTTATTCTCAGAATATGAAAATTAAATGTGTCATTAATATTCTAGAGAG  
TAA

327/615

**FIGURE 324**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pi: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPVV
HPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWS
DMVTLKARMNTNYGLPRYRWLTHAWNFFQREFKCCGVYYFTDWLEMTEMDWPPDSCCVREFPGC
SKQAHQEQLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDR
REPGTDQMSLKDNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

328/615

**FIGURE 325**

AGCAGTGCATTGCTGGAGCGAGGAGAAGCTCACGAATCAGCTGCAGGTCTGTTTGAAAAAA  
GCAGAGATAACAGAGGCAGAGGAAAAGGGTGGACTCCTATGTGACCTGTTAGAGCAAGACA  
ATCACCACATCTGAATTCCAGAACGCCCTGTTCATGGTGGGGATATTCCTCGACTGC**ATG**GAAT  
CAGAAAGAAGCAAAGGATGGGAAATGCCCTGCATTCCCCTGAAAAGAATTGCTTATTCCTAT  
GTCTCTTATCTGCCTTGTGACTGAGGGAGAAACAGCGAAGCCAAATGCCCTGCCG  
TGTGTACTGTACCAAAGATAATGCTTATGTGAGAATGCCAGATCCATTCCACGCACCGTTC  
CTCCTGATGTTATCTCATTATCCTTGTGAGATCTGGTTACTGAAATCTCAGAAGGGAGTT  
TTTATTACGCCATCGCTGCAGCTCTGTTATTACATCGAACTCCTTGATGTGATCAGTG  
ATGATGCTTTATTGGTCTTCCACATCTAGAGTATTATTCATAGAAAACAACAATCAAGT  
CAATTCAAGACATACTTCCGGGGACTAAAGTCATTAATTCACTTGAGCCTGCAAACAACA  
ATCTCCAGACACTCCAAAAGATATTCAAAGGCCTGGATTCTTAACAAATGTGGACCTGA  
GGGTAATTCAATTGACTGAAACTGAAATGGCTAGTGGAAATGGCTGGCCACACCA  
ATGCAACTGTTGAAGACATCTACTGCGAAGGCCCGAGAATACAAGAAGCGAAAATCAATA  
GTCTCTCCCGAAGGATTGCTTCATCATTACAGAATTGCAAAGTCTCAAGACCTGCCTT  
ATCAATCATTGTCATAGACACTTTCTTATTGAATGATGAGTATGATGTCATCGCTCAGC  
CTTTACTGGAAAATGCATTTCTTGAATGGGACCATGTTGAAAAGACCTTCCGGAATTATG  
ACAACATTACAGGCACATCCACTGTAGTATGCAAGCTATAGTCATTGAAACTCAGCTCTATG  
TTATTGTGCCAGCTGTTGGCTCTCACATCTATAAGCGAGACAGTTGCAAATAAT  
TCATAAAAATCCAGGATATTGAAATTCTCAAAATCCGAAAACCCAATGACATTGAAACATTCA  
AGATTGAAAACAACGGTACTTGTGCTGACAGTTCAAAGCTGGTTTACTACCATTAC  
AAATGGAACGGAAACGGATTCTACTCCCATCAATCCTACACGCGTGGTACAGGGACACTGAT  
GTGGAATATCTAGAAATAGTCAGAACACCTCAGACACTCAGAACGCCTCATTAATTCTGTCT  
AGTAGTCCCAGCGCTCTGTAATTTCAGTGGAAACAAAGCAACACAATTTCACTAACCAA  
ACTGACATCCTAACATGGAGGATGTGACTGCGAGTGAAGCACTTCTCAGTGAAGGGACGTG  
TACATTGCTTGACAAGATTCTGGTGAATTCCAAAGTCATGAAATGGGAGGCTCTCGTTC  
CAGGATATTCAAGAGGATGCCATCGCGAGGATCCATGGTGTCCAGCCTCTCAAATAATAAT  
TACCAATATGCAATTCTGGAAGTGTACTCCTTACTCAAGTGTATAACTGGGATGCAGAG  
AAAGCCAAATTGTAATTCAAGGAATTAAATGTTCAAGGCACCAAGATCATCACACATGTG  
TCCATTAAAGCGTAATTCTTTGCTCCAGTTAAGGGAAATACACAGATTACAAA  
CATGTCATAGTTGACTTAAGCGCA**TGAG**ACACCAAATTCTGGCTGCCATCAGAAATTCT  
ACAGTACATGACCCGGATGAACATCAATGCATGATGACTCTTCTTATCACACTGCAAATGAAT  
GCCTTCAAACATTGAGACTGCTAGAACCAAGCAACTACCAGTATCTCCATCCTTAACGTCCA  
GTCCAGTGTGGAGTTACCTTATAAGACAAAATTAAATTGTGTAACGTGTTCTTGCA  
GTGAAGATGTGAAATAAGCGTTAATGGTATCTGTTACTCCAAAAGAAATATTATGTA  
CTTTCCATTATTATTACATGTGACAGAACACTGCCAAATAATGTTACATTCTT  
TCATA

329/615

**FIGURE 326**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68882
><subunit 1 of 1, 557 aa, 1 stop
><MW: 63818, pI: 8.61, NX(S/T): 3
MESERSKRMGNACIPLKRIAYFLCLLSALLTEGKKPAKPCKPAVCTCTKDNALCENARS
IPRTVPPDVISLSFVRSGFTEISEGSFLFTPSSLQLLLFTSNSFDVISDDAFIGLPHLEYL
FIENNNIKSISRHTFRGLKSLIHLSIANNLQTLPKDIFKGLDSLTNVDLRGNSFNCDCK
LKWLVEWLGHNTATVEDIYCEGPPEYKKRKINSLSHKDFDCIITEFAKSQDLPYQSLSID
TFSYLNDEYVVIAQPFTGKCIFLEWDHVEKTFRNYDNITGTSTVVCKPIVETQLYVIVA
QLFGGSHIYKRDSFANKFIKIQDIEILKIRKPNDIETFKIENNWyFVVADSSKAGFTTIY
KWNGNGFYSHQSLHAWYRDTDVEYLEIVRTPQTLRTPHLILSSSSQRPVIYQWNKATQLF
TNQTDIPNMEDVYAVKHFSVKGDVYICLTRFIGDSKVMKGSSFQDIQRMPSRGSMVFQ
PLQINNYQYAILGSDYSFTQVYNWDAEKAKFVKFQELNVQAPRSFTHVSINKRNFLFASS
FKGNTQIYKHVIVDLSA
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-34

**Transmembrane domain:**

Amino acids 281-306

**N-glycosylation sites:**

Amino acids 192-196; 277-281; 422-426

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 310-314

**Tyrosine kinase phosphorylation sites:**

Amino acids 228-235; 378-385

**N-myristoylation sites:**

Amino acids 172-178; 493-499

**Amidation site:**

Amino acids 33-37

330/615

**FIGURE 327**

CCAAGGCCAGAGCTGTGGACACCTTATCCACTCATCCTCATCCTCTGATAAAGCCC  
CTACCAGTGTGATAAAAGTCTTCTCGTAGAGGCCTAGAGGCCTAAAAAAAAGTGCTTGA  
AAGAGAAGGGGACAAAGGAACACCAGTATTAGAGGATTTCCAGTGTCTGGCAGTTGGTC  
CAGAAGGATGCCTCCATTCTGCTTCTCACCTGCCTCTCATCACAGGCACCTCCGTGTCA  
CGTGGCCCTAGATCCTGTTCTGCTTACATCAGCCTGAATGAGCCCTGGAGGAACACTGACCA  
CCAGTTGGATGAGTCTCAAGGCCTCCTCTATGTGACAACCATGTGAATGGGGAGTGGTACCA  
CTTCACGGGCATGGCGGGAGATGCCATGCCTACCTCTGCATACCAGAAAACCACTGTGGAAC  
CCACGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCAGGGCATTGTGCAACGCCA  
GGCTTGTGCCAGCTCAATGGGAACGCTGTCTGGAACACCACGGTGGAAAGTCAAGGCTG  
CCCTGGAGGCTACTATGTGTATCGTCTGACCAAGCCCAGCGTCTGCTCCACGTCTACTGTGG  
TCATTTTATGACATCTGCGACGAGGACTGCCATGGCAGCTGCTCAGATACCAGCAGTCAC  
ATGCGCTCAGGAACGTGCTAGGCCCTGACAGGCAGACATGCTTGATGAAAATGAATGTGA  
GCAAACAAACCGTGGCTGCAGTGGATCTGTGTGAACCTCAAAACTCCTACCGCTGTGAGTG  
TGGGGTTGCCGTGTGCTAAGAAGTGTGGCAAGACTGTGAAGACGTTGAAGGATGCCACAA  
TAACAATGGTGGCTGCAGCCACTCTGGCTTGGATCTGAGAAAGGCTACCGTGTGAATGTCC  
CCGGGGCCTGGTGTCTGAGGATAACCACACTTGCCTGCTGGTGGCTGGAGCTCTCCTGAC  
TGCATTGAAGTGAACATCCCCAGGGAGCTGGTGGCTGGAGCTCTCCTGACCAACAC  
CTCCTGCCAGGGAGTGTCCAACGGCACCCATGTCAACATCCTCTCTCAAGACATGTGG  
TACAGTGGCGATGTGGTGAATGACAAGATTGTGCCAGCAACCTCGTGACAGGTCTACCCAA  
GCAGACCCCCGGGAGCAGCGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCCTGAC  
CTGCGAGTTCCACGCCTGTACACCATTCTGAAGGATAACGTTCCAAACCTTCGAAACTCCCC  
ACTGGAATCATGAGCCGAAATCATGGGATCTTCCATTCACTCTGGAGATCTCAAGGACAA  
TGAGTTGAAGAGCCTACGGGAAGCTCTGCCACCCCTCAAGCTCGTGACTCCCTCTACTT  
TGGCATTGAGCCGTGGTCACGTGAGCGGCTTGGAAAGCTTGGTGGAGAGCTGCTTGGCAC  
CCCCACCTCCAAGATCGACGAGGTCTGAAATACTACCTCATCCGGATGGCTGTGTTCA  
TGACTCGGTAAAGCAGTACACATCCCAGGATCACCTAGCAAAGCACTTCCAGGTCCCTGTCTT  
CAAGTTGTGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGTTCTGTCTGTGGAGT  
GTGGACGAGCGTCCCGCTGTGCCAGGGTGGCCACCGCGAATGCGTGTGGCAGGGAG  
AGAGGACTCAGCCGGTCTACAGGGCCAGCGCTAACAGGCCCGATCCGCATCGACTGGGA  
GGACTAGTTCGTAGCCATACCTCGAGTCCCTGCATTGGACGGCTTGCTCTTGGAGCTTCTC  
CCCCCACCGCCCTCTAAGAACATCTGCCAACAGCTGGGTCAGACTTCACACTGTGAGTTGAG  
ACTCCCAGCACCAACTCACTGTGATTCTGGCATTCACTGGGACAGGTACAGCACTGCTG  
AACAAATGTGGCCTGGTGGGTTCATCTTCTAGGGTTGAAAACAAACTAAACTGTCCACCCAGAA  
AGACACTCACCCATTCCCTCATTTCTTCAACTAAATACCTCGTGTATGGTGCATC  
AGACCACAAAATCAGAAGCTGGGTATAATATTCAGTTACAAACCTAGAAAAATTAAACAG  
TTACTGAAATTATGACTTAAATACCAATGACTCCTTAAATATGTAAATTATAGTTACCTT  
GAAATTCAATTCAAATGCAGACTAATTATAGGAATTGGAGTGTATCAATAAAACAGTAT  
ATAATT

331/615

**FIGURE 328**

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFT  
GMAGDAMPTFCIPEHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCLWNNTVEVKACPG  
GYYVYRLTKPSVCFHVYCGHFYDICDEDCHGSCSDTSECTCAPGTVLGPDRTCFDENECEQN  
NGGCSEICVNLKNSYRCECGVGRVLRSDGKTCEDVEGCHNNNGCASHSCLGSEKGYQCECPRG  
LVLSEDNHTCQVPVLCKSNAIEVNIPRELVGGLEFLTNNTSRGVSNHGTHVNILFSLKTCGTV  
VDVVNDKIVASNLVTGLPKQTGSSGDFIIRTSKLLIPVTCEFPRLYTISEGYVPNLRNSPLE  
IMSRNHGIFPFTLEIFKDNEFEPPYREALPTLKLRDSLFGIEPVHVSGLESLVESCFATPT  
SKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHEVFLHCRVLVCGVLD  
ERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

332/615

**FIGURE 329**

GAGAGAGGCAGCAGCTTGTCAAGCGGACAAGGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCT  
GCACTCGGGCCTCCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACC  
TGTGTGGGGAGGCCCTCCTGCTGCCTGGGTGACAATCTCAGCTCAGGCTACAGGGAGACC  
GGGAGGATCACAGAGCCAGC**ATGTT**ACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCG  
ATGTCAAACCCCTGCGCAAACCCCCTGATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCA  
TCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTTGCTCATCAAGGTGATT  
TGGATAAAACTACTTCCTCTGGGGCAGCCTCCACTCATCCGAGGAAGCAGCTGTGTG  
ACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTCCCCGAAG  
GCCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCA  
CAGGGAACTGGTTCTCTGCCTGTTGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTA  
GGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGATGTTGAAA  
TCACAGAAAACAGCCAGGAGCTCGCATCGGAACTCAAGTGGGCCCTGTCTCAGGCTCCC  
TGGTCTCCCTGCACTGTCTGCCTGTTGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGG  
AGGAGGCCCTGTGGATTCTGGCCTGGCAGGTCAGCATCCAGTACGACAAACAGCACGTCT  
GTGGAGGGAGCATCTGGACCCCCACTGGTCCTCACGGCAGCCACTGCTTCAGGAACATA  
CCGATGTGTTCACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGCAGCTCCATCCCTGG  
CTGTGGCCAAGATCATCATATTGAATTCAACCCATGTACCCAAAGACAATGACATGCC  
TCATGAAGCTGCAGTCCCACTCATTCTCAGGCACAGTCAGGCCATCTGTCTGCCCT  
TTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATGGATGGGCTTACGAAGCAGA  
ATGGAGGGAAAGATGTCTGACATACTGCTGCAGGCAGTCCAGGTATTGACAGCACACGGT  
GCAATGCAGACGATGCGTACCGAGGGAAAGTCACCGAGAAGATGATGTGTGCAGGCATCCGG  
AAGGGGGTGTGGACACCTGCCAGGGTGACAGTGTTGGCCCTGATGTACCAATCTGACCGAT  
GGCATGTGGTGGGCATCGTTAGCTGGGCTATGGCTGCAGGGGGAGCAGGCCAGGAGTAT  
ACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG**TAATGCT**  
GCTGCCCTTGCACTGCTGGAGGCCCTCCCTGCCCTGCCACCTGGGATCCCCAA  
AGTCAGACACAGAGCAAGAGTCCCCTGGGTACACCCCTGCCCACAGCCTCAGCATTTCTT  
GGAGCAGCAAAGGGCCTCAATTCTGTAAGAGACCCCTCGCAGCCAGAGCGCCAGAGGAAG  
TCAGCAGCCCTAGCTCGGCCACACTGGTGCTCCAGCATCCCAGGGAGAGACACAGCCACT  
GAACAAGGTCTCAGGGTATTGCTAACGCAAGAAGGAACCTTCCACACTACTGAATGGAAGC  
AGGCTGTCTGTAAAAGCCAGATCACTGTTGGGCTGGAGAGGAAGGAAAGGGTCTCGGCCA  
GCCCTGTCCGTCTCACCCATCCCCAAGCCTACTAGAGCAAGAAACCAGTTGTAATATAAAAT  
GCACTGCCCTACTGTTGGTATGACTACCCTACTGTTGTCATTGTTATTACAGCTATGG  
CCACTATTATAAGAGCTGTGTAACATCTGGCAAAAAAAAAAAAAA

333/615

**FIGURE 330**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pi: 5.18, NX(S/T): 2
MLQDPDSQQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIVVVIKVILDKYYFL
CGQPLHFIPRKQLCDGEELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSA
CFDNFTEALAEATACRQMGYSRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSLHCL
ACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWLTAHCFRKHTDVFNWK
VRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTSGTVRPICLPFFDEELTP
ATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDT
QGDGGPLMYQSDQWHVVGIVSWGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

**Transmembrane domain:**  
amino acids 32-53 (typeII)

334/615

**FIGURE 331**

AGTGGTTCGATGGGAAGGATCTTCTCCAAGTGGTCCTCTGAGGGGAGCATTCTGCTGGC  
TCCAGGACTTGGCCATCTATAAAGCTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGACG  
AGCTCTGAGTGAGACCCACAAGCTGCTTCAACAAATTGCAATGGAGCCTTCGAAATCA  
ATGTTCAAAGCCCCAAGAGGAGAAATGGGGTGAACCTCTCCCTAGCTGTGGTGCATCTACC  
TGATCCTGCTCACCGCTGGCGTGGCTGGTCCAAGTCTGAATCTGCAGGCGCGC  
TCCGGGTCTGGAGATGTATTCTCAATGACACTCTGGCGGCTGAGGACAGCCCCTCCTCT  
CCTGCTGCAGTCAGCACACCCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTGCAAGTCC  
TGCAGGCCAACTCACCTGGTCCGCGTCAGCCATGAGCACTGCTGCAGGGTAGACAAC  
TCACTCAGAACCCAGGGATGTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTCTCAAGGTC  
ACAAGGGGGCATGGCATGCCCTGGCCGCCCCGACACCTGCTGAGAACAGGGAG  
CCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCGGGACCCAAAGGCCACCGGGAG  
TCAAGGGAGAGGCGGGCTCCAAGGACCCCAGGGTGCTCCAGGAAGCAAGGAGCCACTGGCA  
CCCCAGGACCCAAAGGAGAGAACAGGCAGCAAAGGCATGGGGTCTCATGGCCAAAAGGG  
AAACTGGAACTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAAAGGGACAGGGCA  
TGAAAGGAGATGCAGGGTCTGGGCTCTGGAGCCAGGGAGTAAAGGTGACTTCGGGA  
GCCAGGCCACCAGGTTGGCTGGTTCTGGAGCTAAAGGAGATCAAGGACAACCTGGAC  
TGCAGGGTGTCCGGGCCCTCTGGTGCAGTGGACACCCAGGTGCCAAGGGTGAGCCTGGCA  
GTGCTGGCTCCCTGGCGAGCAGGACTCCAGGGAGGCCAGGGAGTCCAGGAGCCACAGGCC  
TGAAAGGAAGCAAAGGGACACAGGACTCAAGGACAGCAAGGAAGAAAAGGAGAATCAGGAG  
TTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGAGGCCAGGGCTGGCAGGTCCAAGGGAG  
CCCCTGGACAAGCTGCCAGAACAGGGAGACCAGGGAGTGAAGGATCTCTGGGAGCAAGGAG  
TAAAGGGAGAAAAGGTGAAAGAGGTGAAAACACTCAGTGTCCGTAGGATTGTCGGCAGTAGTA  
ACCGAGGCCGGCTGAAGTTACTACAGTGGTACCTGGGGACAATTGCGATGACGAGTGGC  
AAAATTCTGATGCCATTGTCTCTGCCCATGCTGGTTACTCCAAAGGAAGGCCCTGTACA  
AAGTGGGAGCTGGCACTGGCAGATCTGGCTGGATAATGTTAGTGTCCGGGCACGGAGAGTA  
CCCTGTGGAGCTGCACCAAGAATAGCTGGGCCATCATGACTGCAGCCACGAGGAGGACGCAG  
GCGTGGAGTGCAGCGTCTGACCCGGAAACCCTTCACTTCTGCTCCCGAGGTGTCCCTCGGG  
CTCATATGTGGGAAGGCAGAGGATCTGAGGAGTTCCCTGGGACAACGTGAGCAGCCTCTGG  
AGAGGGGCCATTAATAAGCTAACATCATTGA

335/615

**FIGURE 332**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886  
><subunit 1 of 1, 520 aa, 1 stop  
><MW: 52658, pI: 9.16, NX(S/T): 3  
MRNKKILKEDELLSETQQAAFHQIAAMEPFEINVPKPKRRNGVNFSLAVVVIYLLTAGAGLL  
VVQVLNLQARLRVLEMYFLNDTAAEDSPSFSLQSAHPEHLAQGASRLQVLQAQLTWVRVS  
HEHLLQRVDNFTQNPQMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRDGAT  
GSPGPQGPPGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGGLIGPKGETGTKGEKDL  
GLPGSKGDRGMKGDAVMGPPGAQGSKDFGRPGPPLAGFPGAKGDQGQPGLQGVPGPPGAV  
GHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDTGLQGQQGRKGESGVPGPAGVKGEQ  
GSPGLAGPKGAPGQAGQKGDQGVKGSSGEQGVKEKGERGENSVSRIVGSSNRGRAEVYYSG  
TWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVAGTGQIWLDNVQCRGTESTLWSCTKNSWG  
HHDCSHEEDAGVECSV

**Transmembrane domain:**

amino acids 47-66 (type II)

**N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 432-440

**N-myristoylation sites.**amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521**Amidation site.**

amino acids 360-364

**Leucine zipper pattern.**

amino acids 56-78

**Speract receptor repeat**

amino acids 422-471, 488-519

**C1q domain proteins.**

amino acids 151-184, 301-334, 316-349

336/615

**FIGURE 333**

GGGCTGTTGATTGTGGGGATTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCTG  
CCTCTGGCATATGCACACACTCACACATTCTGTCACACCGTCACACACATACCATGTTCT  
CCATCCCCCAGGTCAGCCCTCAGTGTGTCACCCATCCAGCAGGGTACCCCTGAAGCTCTGGC  
TGCAGCCCCCTCCCGTCCAGTGGCAGGGCCTTCATCCCTCTTCTCTCCAAAGCCAACTG  
CTGTCAGTGCATGCTCTGCCAAGGAGGAGGAACAGCAGTGACAGCAGGAGTAAGAGTGGAG  
GCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGTTCAGCGAGCCTAGAGAGGGCAGACTA  
TCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAAGAGGGCAGAACCGG  
GGCACTTGTGGGTTGCAGAGCCCCTCAGCCATGTTGGGAGCCAAGGCCACACTGGCTACCAGGT  
CCCCTACACAGTCCCAGGCTGCCCTTGGTTCTGGTCTCTGGCCCTGGGGCCGGTGGGCC  
CAGGAGGGGTCAAGAGCCCCTGCTGGAGGGGAGTGCCCTGGTGGTCTGTGAGCCTGGCCGA  
GCTGCTGAGGGGGCCGGGGAGCAGCCCTGGGAGAGGCACCCCCCTGGCGAGTGGCATT  
GCTGCGGTCGAAGCCACCACCATGAGCCAGCAGGGAAACCGGCAATGGCACCACTGGGCC  
ATCTACTTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTGACCCGGCTCTGGCTCTTC  
GTAGCCCCGTCCGGGGTGTCTACAGCTTCCGGTCCATGTGGTGAAGGTGTACAACGCCAA  
ACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCTGTCTAGCAGCCTTGCCAATGATCCT  
GACGTGACCCAGGAGGCAGCCACCAGCTGTGCTACTGCCCTGGACCCCTGGGACCGAGTG  
TCTCTGCCTCGCTGGGGAAATCTACTGGTGGTGGAAATACTCAAGTTCTGCTGGCTTC  
CTCATCTTCCCTCTTGAGGACCAAGTCTTCAAGCACAAGAATCCAGCCCCTGACAACCTT  
CTTCTGCCCTCTTGTCCCCAGAAACAGCAGAGGCAGGAGAGACTCCCTGGCTCTATC  
CCACCTCTTGCATGGGACCCGTGCCAAACACCAAGTTAAGAGAAGAGTAGAGCTGTGGC  
ATCTCCAGACCAGGCCTTCCACCCACCCACCCAGTTACCCCTCCAGGCCACCTGCTGCATC  
TGTTCCTGCCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCAAGAAGGAAGATCTGCACTACTT  
TGCAGCAGGTGAGCCTGACAGGCCACAGGAGCCAGATGGACAAGCCTCAGCGTACCCCTG  
CAGGCTTCTTCTGTGAGGAAAGCCAGCATCAGGATCTCAGCCAGCACCGTCAGAAGCTGAG  
CCAGCACCGTATGGCTAGGGTGGGAGGCTAGCCACAGGCAGAAGGGTGGGAAGGGCTGGA  
GTCTGTGGCTGGTGGAGGAAGGAAGGAGGGTGTATTGTCTAGACTGAACATGGTACACATTCTG  
CATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCTGGCTGCTCTTCTATGCTGGATCCCAGAT  
GGACTCTGCCCTTACCTCCCCACCTGAGATTAGGGTGAGTGTGTTGCTCTGGCTGAGAGCA  
GAGCTGAGAGCAGGTATACAGAGCTGGAAGTGGACCATGGAAAACATCGATAACCATGCATCC  
TCTTGCTGGCCACCTCCTGAAACTGCTCCACCTTGAAGTTGAACCTTAGTCCCTCCACAC  
TCTGACTGCTGCCCTTCCCTCCAGCTCTCACTGAGTTATCTTCACTGTACCTGTTCCAG  
CATATCCCCACTATCTCTTTCTCTGATCTGCTGTCTTATTCTCCTCCTTAGGCTTCCT  
ATTACCTGGGATTCCATGATTCAATTCCCTCAGACCCCTCTGCCAGTATGCTAAACCCCTCCC  
TCTCTCTTCTTATCCCGCTGCCCATTGGCCAGCCTGGATGAATCTATCAATAAAACA  
AGAGAATGGTGGTCAGTGAGACACTATAGAATTACTAAGGAGAAGATGCCCTGGAGTTGGA  
TCGGGTGTTACAGGTACAAGTAGGTATGTTGCAGAGGAAAATAATCAAACGTATACTAA  
AATTAAAAA

337/615

**FIGURE 334**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180  
><subunit 1 of 1, 205 aa, 1 stop  
><MW: 21521, pI: 7.07, NX(S/T): 1  
MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVILLEGECLVVCEPGRAAAGGPGGAA  
LGEAPPGRAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVYSF  
RFHVVVKVYNRQTVQVSIMLNTWPVISAFANDPDVTREAATSSVLLPLDPGDRVSLRLRRGNLL  
GGWKYSSFSGFLIFPL

**Signal peptide:**  
amino acids 1-32

338/615

**FIGURE 335**

339/615

**FIGURE 336**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184  
><subunit 1 of 1, 388 aa, 1 stop  
><MW: 43831, pI: 9.64, NX(S/T): 3  
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWTGSSILSALQDLFSVTWLNRSK  
VEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVDWNTPKKGRRSQW  
VRNWAVWRYFRDYFPIQLVKTHNLLTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFPGIR  
PYLATLAGNFRMPVLREYLMGGICPVSRDTIDYLLSKNGSGNAAIIIVVGAAESLSSMPGKN  
AVTLRNKRGFVKLALRGADLVPIYSFGENEVYKQVIFEEGSWGRVQKKFQKYIGFAPCIFH  
GRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDKHKTFG  
LPETEVLEVN

**Important features of the protein:**

**Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-  
245, 318-323, 378-383

340/615

**FIGURE 337**

GGGGCGGGGATGGGGGCCGGGGCGGGCGCCGACTCGCTGAGGCCCGACGCAAGGCCGGGCCGGGG  
GGGCCGAGGAGCGCGGCCAGAGCAGGGCGAGGCAGGCCGGGGACGCCCGCGACGAGCAGGTGGC  
GCGGCTGCAGGCTGTCCAGCCGAAGGCCCTGAGGGCAGCTGTTCCACTGGCTCTGCTGACCTTGTGCCTTGG  
CGGCTGCTCAGCGAGGGGCCGTGACCCGCTCTGAGCAGCGCCATGGGCTGCTGGCTTCTGAAGACCCA  
GTCGTGCTGACCTGCTGGCTGGCTTGTCTCGTGGTAGTGGCTGGCATCAACTTCGTCAGCTGTGCAC  
GCTGGCGCTCTGGCGGTGAGCAAGCAGCTTACGCCGCTCAACTGCCCTGCCACTCACTCTGGAGCCA  
ACTGGTCATGCTGCTGGAGTGGTCTGACGGAGTGTACACTGTTACGGACCAGGCCACGGTAGAGCGCTT  
TGGGAAGGGAGCACCGAGTCATCATCCTCAACCACAACCTCGAGATCGACTCCTCTGTTGGGAGGACCATGTGTGA  
GCGCTTGGAGTGTGGAGCTCAAGAGTCTCGTAAGAAGGAGCTGCTCTACGTGCCCCCTCATGGCTGGAC  
GTGGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG  
GCGCCTGCGACTACCCCAGTACATGTTCTCCTGTACTCGAGGGGACGCGCTCACGGAGAACCAAGCA  
CCGCGTAGCATGGAGGTGGCGCTGCTAAGGGCTTCTCTGCTCAAGTACACCTGTCGCCGGGACCAAGGG  
CTTCACACCGCAGTCAGTGCTCCGGGGACAGTGCAGCTGTCTATGATGTAACCTGAACCTCAGAGAAA  
CAAGAACCGTCCCTGCTGGGGATCCTCTACGGGAAGTACGGAGCGACATGTGCGTAGGGAGATTCCCT  
GGAAGACATCCCCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAAGGAGAACGCGCTCCA  
GGAGATATATAATCAGAAGGGCATGTTCCAGGGGAGCAGTTAACGCTGCCGGAGGCCGTGGACCCCTCTGAA  
CTTCCTGCTGGGCCACCATTCTCTGTCCTCCCTCTCAGTTGTCTGGCGTCTTGCACGGGATCACC  
TCTCTGATCCTGACTTTCTTGGGTTGTGGAGCAGCTTCTGGAGTTCGCAAGACTGATAGGAGAATCGCT  
TGAACCTGGAGGTTGAGATTGCACTGAGCTGAGATGGCATCACTGTAACCTCAGCCTAGGCAACAGAGCAAGACT  
CAGTCTCAAAAAAAAAAAAAACAAAAACCCCAGAAATTCTGGAGTTGAACTGTGTAGTTACTGACATGAAAA  
ATTCACTAGAGGCTAACAGCAGATTGAGCAGGCAGAAAAAAATCAGCAAGCTGAAAGATGGTACCTTGAGATT  
TTTCAGGCTAATGAAAAAGAATGAAGGAAATTAAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA  
CATATGCACTGAGAGTCCCAGAAGGGAGAGAACGGGTCAAGAAAGAATGCCACAAGCTGATGAAAACA  
GTAACCTACCCACTCAGGAAGCTAGTAACTCAGGATGAATATCAGAGATGCCACACCTAGATATTCTCAT  
AATCAAAGTGTCAAATGACAAGAATTCTGGAAAGCAGCAAGAGATGAGCAACTTATCTGTTCAAAGGACTTTG  
ATCAGATTAACAGCTCATTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAAACACTGTTGAAAGGAA  
AACCTCAACTGAAATTATTGGACTTTGAGCTTCTAGATGGTCTGACCTCTTGTCTCAGGGACAGTTTCA  
ATTTAATCCCTAATAACAATTAGTCAGCTTCTGACCTGAGGAAGGCCGTGCTTAGGCCGGCACAGTGGC  
TTACACCTGTAATCCCAGCATTGGGAGGCCAGACGGGTGGATCATTGGGCTAGGCTGATCTCAAACCTCT  
GAGTCAGGTGATCTGCCGCCTCAGCCTCCAAAGTGTGTGATTGCAAGGCGTCAAGGCACTGCCCTGGCCGGA  
ATTTCTTTAAGGTGAATGAGGGGCCAGGCAGATGGCTACGCCGTGATCCCAAGTAGCTTGGATTGTA  
AACATGCAACCACTGCCGTAAATTGTTGATTTTGTAGTAGAGACGTGTTAGCCAGGCTGGCTCGATCTCCT  
GACCTCAAGTGCACACCTGCCCTCAGCCTCCAAAGTACTGGGATTACAGGCGTGAAGCCACTGTGCTGCCCTTGA  
GCATCTGTGATGTCATTGGCATTGTTGATATCTCTATCTTGGGAAATGTCGTTCAAAGTCTTGG  
CCTTTAAATTGTTATTATTATTATTGAGACAGGGCTCTGTTCTGCTGCCAGGCTGGAGT  
CAGTGGCACAGTCTGGCTACTGCAGCCTCGACCTCTGGCTGAGTGAATCTCCACACTCAGCCTCCCTTGT  
AGCTGTTATTGTTGTTGATTTGAGCTGAGTGTAGTTTGTGTTGAGAGACGATTTCACCATG  
TGCCCAGGCTGGTCTGAACCTCTGAGCTCAAGTGAATGTCGCTCTGAGCTCCTCAAAGTGTGGGATTACAGA  
CATGAGGCCACTGCACCTGGCAAACCTCCAAAATTCAACACACACACACACACACACACACACACACACAC  
GAGGGGCCGGGTGTGGCCCAACTACCAGGGAGACTGAAGTGGGAGGATGCCCTGGGATGAGAAGTCAGGCGT  
CAGTGAAGTCAGGTTGTGCACTGCATTCCAGCCTGGACAAACAGAGTGAAGACCCCTGTC

341/615

**FIGURE 338**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pi: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVSGLVINFVQLCTLALWPVKQLYRRLNCRAYSLWSQLVM
LLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEDFLCGWTMCERFGVLGSSKVLAKKEL
LYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSM
EVAAAKGLPVLYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKKYEAD
MCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIQYNQKGMFPGEQFKPARRPWTLLNFLSWA
TILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRLIGESLEPGRWRLQ
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169

342/615

FIGURE 339

GATATTCTTATTAAAGAATCTGAAGTACTATGCACTCCCTCCAATGTCCGGGGCAG  
CCACCAGGCATATTCATCTTGTGTGTTTCTTTGCTTAGCACTGGGGCACTTCTTGC  
TTATTCTTGGTAGGAAAGGGCTCAGTTGTCTGTGGGTTGGCAGGCAGGCCGGCT  
TACGCCTGATAACGCCCTGGGTTAGAAGGGAAAGGATAAAACTTTAACAAATGGGGATA  
GCTGGGGTCTGAGACCTGCTCCTCAGTAAAATTCCCTGGGATCTGCCTATACCTCTTCTC  
TAACCTGGCATAACCCCTGCTAAAGCCTCTCAGGGCTTCTCTGTCTTAGGATCAAAGTATT  
TAGAGCTACAAGAGCCCTATGGTCTGGCCCTGCCCTGGCCAGCTTCATTGTACATGTG  
GTGTTCTTGTGCGTTCTGTAATGTGGTATGCCATGGGTCTTGACACAAGCCTTCCTCTT  
TGGCTGGACACTGTCCTGCCCTGGCCCCCCTACTCTCCTACTTAATATGTAGTCATCCTGCAG  
ATTTCAATTCTAACATCATTCTCCAGGGATCTGGCCTGACAGAATCTCATCTGTTAAT  
GCTCTCATAAAGACCACTTGTCTCCCTTTGCAGCACCTGCCACTCAGTTGTATCTTATGTG  
GTTTGTGGTTGTATGGGTTGTCTGTTCCCAGAATGCCAGCTCTGAGCTGCGTGAGGGTC  
AAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCTCATGTTTAGAGA  
CTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCAAGATGGTGTAGGGCC  
CAGCATTGTAATTACACGTTGACTGTGCTTGTGAATTATCTGGGATGCAGGTCTGATT  
AGTAGGCCAGGTTGGGCATCTCTAACAAACTCCCACGTGATGCTGATGCTGGCCTATGAAC  
TATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGCATGGTGGCTCACACCTATGATCCC  
GCACCTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATTCAAGACTAGCCTGGCCA  
ACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTGGCATGGTGGCACATGCC  
GTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTGAACCTGGGAGGCGGAGGTTG  
CAGTGAGGCCAGGACTGTTCAACCAGGGTACAGAGTGAGACTCTATGTCCAA  
AAAAAAAAAA

343/615

**FIGURE 340**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234  
><subunit 1 of 1, 143 aa, 1 stop  
><MW: 15624, pI: 9.58, NX(S/T): 0  
MHHSLQCPGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSGVGGRQAGLRLIRPWVRRE  
GKINFYTNNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPEPSWSGP  
CPPGQLHCTCGVLLSFL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

344/615

**FIGURE 341**

CGCCATGGCCGGCTATCCGCGGGTCCGCGCGCAGTGCTCGCCGCCCTGCTGGCGTCGACG  
CTGTTGGCGCTGCTCGTGTGCCCCGCGCGGGTGCAGGGCCGGGACACGGGGACTGGGAC  
GAGGCCTCCCGGCTGCCGCCGCTACCACCCCGCGAGGACGCGCGCGCGTGGCCCCTCGTG  
ACGCACGCTCTCCGACTGGGGCGCTCTGGCCACCATCTCACGCTGGAGGCAGGCGTGCAGGGCCGG  
CCCTTCGCCGACGTCCCTCGCTCAGCGACGGGGCCCCGGCGCGGGCAGCGCGTGCCTAT  
TTCTACCTGAGCCCCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTACACTG  
ACCATGACTTGGCACAGACCAACTCTGCAAGAAACATGGATTGATCCACAAAGTCCCCTT  
TGTGTTCACATAATGCTGTCAGGAACGTGACCAAGGTGAATGAAACAGAAATGGATATTGCA  
AACGATTGTTATTGATTGACACCCCTGAGATGAAAACCTGGCCTTCCAGCCATAATTGGTTC  
TTTGCTAAGTTGAATATAACCAATATCTGGGTCTGGACTACTTGGTGGACCAAAATCGTG  
ACACCAGAAGAATATTATAATGTCACAGTCAGTGAAGCAGACTGTGGTGAATTAGCAACAC  
TTATGAAGTTCTTAAAGTGGCTCATACACACTAAAAGGCTTAATGTTCTGGAAAGCGT  
CCCAGAATATTAGCCAGTTCTGTC

345/615

**FIGURE 342**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269  
><subunit 1 of 1, 220 aa, 1 stop  
><MW: 24075, pi: 7.67, NX(S/T): 3  
MAGLSRGSRALLAALLASTLLALLVSPARGRRGRDHGDWDEASRLPPLPPREDAARVAR  
FVTHVSDWGALATISTLEAVRGRPFADVLSSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN  
PYATLTMTLAQTNFCKKHGFDPQSPLCVHIMLSGTVTKVNETEMDIAKHSLFIRHPEMKT  
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTQ

**Important features of the protein:**

**Transmembrane domain:**

Amino acids 11-29

**N-glycosylation sites:**

Amino acids 160-164;193-197;216-220

**N-myristoylation sites:**

Amino acids 3-9;7-13;69-75;97-103

346/615

**FIGURE 343**

GGCTGGACTGGAACCTCTGGCCCCAAGTGATCCACCGCCTCAGCCTCCCAAGGTGCTGTGAT  
TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTCACTAAAGGCCACAG  
GAGTTGAACGTCTAGGATTCTGACTATGCTGTGGTAGTGCTCCTACTCCTACCTACATT  
AAAATCTGTTTTGTTCTCTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGTCACT  
GTGGCTCTGGCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTCTACCCACACCCT  
CCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTGCTGGAGCAGTGCCCTCACCAAC  
TGTCTCACGTCTGGAGGCAGTGACTCGGGCAGTAGCTGAGGCTCTGGTAGTCGG  
CTTCAAGGTGGGCCTGCCCTGGCCGTTAGAAGGGATTGACAAGGCCGAAGATTCATAGGCG  
ATGGCTCCACTGCCACGGCATCAGCCTGCTGAGTCATCACTGCCCCTGGGCCAGGACGG  
GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCGCCATCTAACCTTT  
CATGTCCTGCACATCACCTGATCCATGGCTAACTGAACTCTGCTCCAAGGAACCCAGAGCT  
TGAGTGAGCTGTGGCTCAGACCCAGAAGGGCTGCTTAGACCACCTGGTTATGTGACAGGA  
CTTGCATTCTCCTGGAACATGAGGGAACGCCGAGGAAAGCAAAGTGGCAGGGAAGGAACCTG  
TGCCAAATTATGGGTCAAGAAAAGATGGAGGTGTTGGTTATCACAAGGCATCGAGTCTCCTGC  
ATTCACTGGACATGTGGGGAAAGGGCTGCCGATGGCGATGACACACTCGGGACTCACCTCTG  
GGGCCATCAGACAGCCGTTCCGCCGATCCACGTACAGCTGCTGAAGGGCACTGCAAGGC  
CGATGCTCTCATCAGCCAGGCAGCAGCCAAATCTGCGATCACAGCCAGGGCAGCCGTCTG  
GGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCTCCTCCCTGAGAGGCCCTCTATGT  
CCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGCTAATGGCTCAGTGTGGCCAGGA  
GGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCTGCTGCGAACACGAAATGCCTCCAGT  
AAAGCACAGGCTGAAAATCCCCAGGCAAAGGACTGTGTGGCTCAATTAAATCATGTTCTAGT  
AATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTCAAATGATCTCCAAGGCCCT  
TATAACCCAGGAGACTTGATTGAATTGAAACCCCAAATCCAAACCTAAGAACAGGTGCA  
TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTGGGAGGCCAGGCG  
GGTAGATCACCTGAGGTCAAGACAGCAGCCTGGCAACATGGTGAACCCCTGTCTC  
TACTAAAAATACAAAAAAACTAGCCAGGCATGGGGTGTGCTGTATCCCAGCTACTCGGG  
AGGCTGAGACAGGAGAATTACTGAAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT  
TCAGCCTGAGCAACACAGCGAGACTCTGTCAGAAAAAATAAAAAAGAATTATGGTTATTT  
GTAA

347/615

**FIGURE 344**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277  
><subunit 1 of 1, 109 aa, 1 stop  
><MW: 11822, pi: 8.63, NX(S/T): 0  
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS  
PCWPLAGAVPSPTVSRLAALTRAVQVAEPLGSCGFQGGPCPGRRD

**Signal peptide:**  
amino acids 1-15

348 / 615

**FIGURE 345**

CCGCCGCCAGCCGCTACGCCGCTGCAGCCGCTTCCGCCCTGGGCCTCGCCGTCAAG  
**CATG**CCACACGCCCTCAAGCCCAGGGACTTGGTGTGCTAAGATGAAGGGCTACCCTCACTG  
GCCTGCCAGGATCGACGACATCGCGGATGGCAGCGTGAAGCCCCACCCAACAAGTACCCCAT  
CTTTTCTTGGCACACACGAAACAGCCTTCCTGGGACCCAAGGACCTGTTCCCTACGACAA  
ATGTAAAGACAAGTACGGGAAGCCAACAAGAGGAAAGGCTTAATGAAGGGCTGTGGGAGAT  
CCAGAACAAACCCCCACGCCAGCTACAGCGCCCTCCGCCAGTGAGCTCCGACAGCGAGGC  
CCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGGGGTCAT  
GGCCGTACAGCGGTAAAGGCCACAGCTGCCAGCAGGATGGAGAGCGACTCAGACTCAGA  
CAAGAGTAGCGACAAACAGTGGCCTGAAGAGGAAGACGCCCTGCCTAAAGATGTCGGTCTCGAA  
ACGAGCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCGAAGAGGAGAA  
CTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCTGAGAAGAAAGC  
AGCGGTCCGGCGCCACGGAGGGCCCTCTGGGGGACGGAAAAAAAAGAAGGCGCCGTCAAG  
CTCCGACTCCGACTCCAAGGCCATTGGACGGGCCAACGCTGAGCCGGTGGCCATGGCGCG  
GTCGGCGTCCCTCCTCCTCTCCTCCGACTCCGATGTGTCTGTGAAGAAGCC  
TCCGAGGGGCCAGGAAGCCAGGGAGAACCTCTCCGAAGCCGCCAGGGCGAACCGAAGCC  
TGAACGCCCTCCGTCAGCTCCAGCAGTGACAGTGACAGCGACGAGGTGGACCGCATCAGTGA  
GTGGAAGCGGGCGGACGAGGCGCGAGGCGCAGCTGGAGGCCGGCGAGAGCAGGA  
GGAGGAGCTCGGGCGCTGCGGGAGCAGGAGAAGGAGGAGAAGGAGCAGGCGAGCGGGC  
CGACCGCGGGGAGGCTGAGCGGGCAGCGGGCAGCAGCGGGGACGAGCTCAGGGAGGACGA  
TGAGCCCGTCAAGAACGGGGACGCAAGGGCCGGGCGGGGTCCCCCGTCCCTCTGACTC  
CGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAACGAAATCAGCGAACAGCCGAGTCCCTCAAG  
CACAGAGCCGCCAGGAAACCTGGCCAGAACGGAGAACAGAGTGCAGGCCAGGAGAACAA  
AGCCAAGCCCAGTGAAGGTGGAGCGGACCCGGAAGCGGTCCAGGGCTCTCGATGGACAGGAA  
GGTAGAGAAGAACAGAGCCCTCCGTGGAGGAGAACAGCTGCAGAACAGCTGAGATCAA  
GTTTGCCTAAAGGTGACAGCCGGACGTGAAGAGGTGCTGAATGCCCTAGAGGAGCTGG  
AACCCCTGCAGGTGACCTCTCAGATCCTCCAGAACACAGACGTGGTGGCACCTTGAAGAA  
GATTGCCCTTACAAAGCGAACAGGACGTAATGGAGAACGGCAGCAGAACAGTCTATACCCGGCT  
CAAGTCGGGGTCTCGGCCAAAGATCGAGGCCGGTGCAGAAAGTGAACAAGGCTGGATGGA  
GAAGGAGAACGCCGAGGAGAACAGCTGGCCGGGGAGGAGCTGGCCGGGAGGAGGCCAGGA  
GAAGGCGGAGGACAAGCCCAGCACCGATCTCTCAGCCCCAGTGAAATGGCGAGGCCACATCACA  
GAAGGGGGAGAGCGCAGAGGACAAGGAGCACAGGAGGGTCCGGACTCGGAGGAGGGCCAAG  
GTGTGGCTCTCTGAAGACCTGCAACGACAGCGTACGGGAGGGTCCGACCTGGACAGGCCTGG  
GAGCGACCCGCAGGAGCGCAGAGGGCACGGGGACTCGGAGGCCCTGGACAGGAGAGCT**TG**  
**A**GCCGCCAGCCAGGCCAGGCCAGCCCCCGCCGAGCTCAGGCTGCCCTCTCCTCCCCGGCTC  
GCAGGAGAGCAGAGCAGAGAACACTGTGGGAACGCTGTGCTGTTGTATTGTCCTGGTT  
TTTTTCTGCCTAATTCTGTGATTCCAACCATGAAATGACTATAAACGGTTTTTA  
ATGA

349/615

**FIGURE 346**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286  
><subunit 1 of 1, 671 aa, 1 stop  
><MW: 74317, pI: 7.61; NX(S/T): 0  
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPNKYPPIFFFTHETAFLGPKDLPYDK  
CKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPVSSSDSEAPEANPADGSDADEDDEDRGVM  
AVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSLDQASVSPSEEEN  
SESSSESEKTSDQDFTEKKAAVRAPIRGPLGGRKKKAPSASDSDSKADSDGAKPEPVAMAR  
SASSSSSSSSSDSDVSVKKPRGRKPAEKPLPKPRGRKP PERPPSSSSDSDSDEVDRISE  
WKRRDEARRRELEARRRREQEEELRLREQEKEEERRERADRGEAERGGSGSSGDELREDD  
EPVKKGRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTE PARKPGQKEKRVPEEKQQ  
AKPVKVERTRKRSEGFSDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELG  
TLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAEEVYTRLKSRLGPKIEAVQKVNKAGME  
KEKAEEKLAGEELAGEEAPQEKKAEDKPSTDLSAPVNGEATSQKGEESAEDKEHEEGRDSEEGPR  
CGSSEDLHDSVREGPDLDLPGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13

350/615

**FIGURE 347**

GTGGGTTCTCCTGGATCTCACCTACCAACTGCAGATCTGGGACTCATCAGCCTCAATAATTATATTAAATTA  
ACACCATTGAAAGAGAACATTGTTCATCATGAATGCTAATAAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA  
TTTCACCTTTCTGCTTGATGATGCTAACGATGACATGACATGTTCTTCCAGTCAGTGGCACTTTGAAGCA  
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTCAAATAGCTGTATTCCCTTTGGGTCATC  
AGAAGGACTGGATTTCAAACTCTCTTAGATGAGGAAGAGGCAGGCTGCTTGGGAGCCAAAGACCACAT  
CTTCTACTCAGTCTGGTGACTTAAACAAAATTAAAGAAGATTATTGGCCTGCTGCAAAGGAACGGGTGGA  
ATTATGTAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTCATCAGAGTACTTCAGCCCTATAACAA  
AACTCACATATGTGTGGAACTGGAGCATTCTACCAATATGTGGGTATATTGATCTGGAGTCTACAAGGA  
GGATATTATATTCAAACACTAGACACACATAATTGGAGTCTGGCAGACTGAAATGCTTCCGATCCTCAGCAGCC  
TTTGCTTCAGTAATGACAGATGAGTACCTACTCTGGAACAGCTCTGATTTCCGGCAAAGATACTGCATT  
CACTCGATCCCTGGGCTACTCATGACCACACTACAGAACTGACATTTCAGAGCACTACTGGCTCAATGG  
AGCAAAATTATTGAAACTTCTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTCTCTTCG  
TGAATCATCTCAAGAACGCAGTACCTCCGATAAAACCATCCTTCTCGAGTTGGAAAGAGTTGTAAGAATGATGT  
AGGAGGACAACGCAGCCTGATAAAACAGTGGAGCAGCTTCTTCTAAGGCCAGACTGATTGCTCAATTCCGGAAAG  
TGATGGGGCAGATACTTACTTTGAGTACCTCAAGATATTATTACTCCCACAAAGAGATGAAAGAAATCTGT  
AGTATATGGAGTCTTACTACAAACAGCTCCATCTTCAAAAGGCTCTGTTGTGTATAGCATGGCTGACAT  
CAGAGCAGTTTAATGGCCATATGCTCATAGGAAAGTCAGACCATCGTGGGTGAGTATGATGGGAGAAT  
TCCTTATCCACGGCCTGGTACATGTCAAAGCAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTCAGA  
TGATGTATCAGTTCATAAAGCGGCACTCTGTGATGATAAGTCCGTATAACCCAGTTGCAAGGAGGACCAACGTT  
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGGATCATGTCATTGCAAGAGATGGCAGTACGA  
TGAATGTTCTGGAAACAGACATTGAACTGCTCTAAAGTTGTCAGCATTCAAAGGAAAAGTGGAAATATGGA  
AGAGGTAGTGTGGAGGAGTTGCAAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATGTCTCTGAAGCA  
GCAACAATTGTACATTGGTCCCGAGATGGATTAGTTCAGCTCTGCAACAGATGCGACACTATGGGAAAGC  
TTGCGCAGACTGTTGCTTGCAGAGACCCCTACTGTGCTGGGATGAAATGCACTGCTCTGATATGCTCCTAC  
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAAATATGGCGACCCAATCACCCAGTGTGGACATCGAAGACAG  
CATTAGTCATGAAACTGTCATGAAAAGGTGATTTGGCATTGAATTAACTCAACCTTCTGGAAATGTATACC  
TAAATCCCAACAAGCAACTTAAATGGTATATCCAGAGGCTACTGATCGAAGTTGCAAGAAGAGGATTCTGGGATGTATTACTG  
TGAAGAACATCATCAAACCGGAAATGGGCTACTGATCGAAGTTGCAAGAAGAAGGATTCTGGGATGTATTACTG  
CAAAGCCCAGGAGCACACTTCATCCACACCATAGTGAAGCTGACTTGAATGTCATTGAGAATGAAACAGATGGA  
AAATACCCAGAGGGCAGACATGAGGAGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATAACAAAGA  
CTACATCCAAATCCTTAGCAGCCAAACTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG  
GAGACAGAGAAACAAGGGGGCCAAAGTGGAAAGCACATGCGAGGAATGAAAGAAGAAACGAAATGAAAGACATCA  
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTATTTCTACTTAATTAAAGAAAATTCCCTTAC  
TATAAAACATTGCCTCTGTTGTATATCCCTTATAGTAATTCAAAATGCTCCCATGGAGTTTGCTAAGG  
CACAAGACAATACTGAATAAGACAATATGTGATGAAATATAAGAAAGGGAAAAATTCAATTGAACCAGTTT  
CCAAGAACAAATCTGCACAAGCAAAGTATAAGAATTATCTAAAAATAGGGGGTTACAGTGTAAATGTTTA  
TGTTTGAGTTGGAAATTATTGTCATGTAATAGTGTAGCTAAGCAAGCCCCGAAATTGATAGTGTATAAGGT  
GCTTATTCCCTGAATGTCATGAAATTACCATGCACTGCTATGCTTATGAAACAGATATA  
CATTCTTATTGAGAACCCAGTACCTGTGAGGCAATTACTCTGGAGAAATGGTATAGGAATTGGAGGGTGCATTATTCTT  
TGGCCACTGGGTTAAATTAGTGTACTACAAACATTGATTACTGAAGGGCACTAATGTTCCCCCAGGTTCT  
ATTGACTAGTCAGGAGTAACAGGTTCACAGAGAGAAGTTGTCAGTTAGTGTGTTTAAAGTATATAACTAA  
GCTCTACAGGGACAGAAATGCTTAATAAAACTTAAAGATATGGAAAATATTAAATAAAACAAGGAAAACA  
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAAGATGGGATTGTTAGAAGACAGAAGGAAAGACAGCCAT  
AAATTCTGGCTTGGGAAAACCTATATCCCATGAAAAGGAAGAACATCACAAATAAGTGGAGAGTAAATGTA  
TGGAGCTTTCACTAGGGTATAAGTAGCTGCCATTGTAATTGTCATTGTTAAAGTATATAAC  
AACTGCTAGCAAATCTGAGGAAACATAAAATTCTCTGAAGAATCATAGGAAGAGTAGACATTATTATAACC  
AATGATATTTCAGTATAATTCTCTTTAAAAAATTATTCATACTCTGTATATTATTCTTTACTGC  
CTTTATTCTCTCTGTATATTGGATTGTTGATTATTTGAGTGAATAGGAGAAACAATAACACACAGA  
GAATTAAAGAAAATGACATTCTGGGGAGTGGGATATATATTGTTGAATAACAGAACGAGTGTAAAATTAAAC  
AACGGAAAGGGTTAAATTAACTCTTGACATCCTCACTCAACCTTTCTCATGCTGAGTTAATCTGTTGTAATT  
GTAGTATTGTTTGTAAATTAAACAATAAAAGCCTGCTACATGT

351/615

**FIGURE 348**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883  
><subunit 1 of 1, 777 aa, 1 stop  
><MW: 89651, pI: 7.97, NX(S/T): 3  
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVGTGTLKQNIPRLKLTYKDLLLSNSCIPFLG  
SSEGLDFQTLLLDEERGRLLLGAKDHIFLSLVDLNKNFKKIYWPAAKERVELCKLAGKDANT  
ECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFDPQQ  
PFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHYIRTDISEHYWLNGAKFIGTFFIPDT  
YNPD-DDK-IYFFFRESSQEGSTS-DKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC-SIPGS  
DGADTYFDELQDIYLLPTRDERNPVYYGVFTTSSIFKGSAVCVYSMADIRAVFNGPYAHKES  
ADHRWVQYDGRIPYPRPGTCPSKYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPVAGGPTFK  
RINV DYRLTQIVVDH VIAEDGQYDVMFLGTDIGTVLKVV SISKEKW NMEEV VLEELQI FKHSS  
IILNMELSLKQQQLYIGSRDGLVQLSIHRCDTYKGACADCLARDPYCAWDGNACSRYAPTSK  
RRARRQDVKYGDPI TQCWDIEDSISHEADEKVIFGIEFNSTFLECIPKSQQATIKWYIQRSG  
DEHREELKPDERIIKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTLNVIENEQMENTQ  
RAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRNKGGPKWKHMQEM  
KKKRNRHHRDLDLDEL PRAVAT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

352/615

**FIGURE 349**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAGCGCAGAGGTATCCTGGAGCATGCCACCAGCGGGGAGCAGA  
 CAACCTCCCAGGTAAAGCTGGAGCAAGACCTGAAGCTGTTCTTCAGGAGCCTGGTGTATTTCACCCCCAC  
 CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTCCTGGAGTGGGGAGCAGAAGGCCTGGCTGGCAAGA  
 GTGGCCTGGAGAAAGAGGTTCAAGCAGGGACTGACCCAGCGAGCTGCCGTGACTACAAGATCCAGAACCATGGC  
 CATC  
 GGGTGAGGTGGGGGGCACAGGTGTATGTGACCTTCTGTCTCAGCAAGAAAGAGCTGAGAGAGGGGATCTGG  
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGAGGGAAAGGTATTAAAGGTAACAGTGTGGCACAAATAGTAA  
 GAGCACAGTTTGGAGCTAGACCACATAGGTTCAAATTCTCTGTGTTCTAGTTCTGTAGCCCCAGGG  
 AAGGGAGTGACTIONACCTCTGGACTTCATTTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT  
 AAGGAAGATAATGACATAATGTATGTGATGCAACTAGCAAAGTACCAAGTCCCAGTAGTAAGTCATGCCACAG  
 TATTCCACCCACCCCTGTTCTGCCTTCCAACCAGGTACTGCAACGACTGGAGCAGAGGGGGCAGCAGGCTT  
 CAGAGCGGGAGGCTCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGACATCCGCCGGGACAGGTGAGCC  
 AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGGCCAGCCA  
 TGACCCAGGGCCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGGCTGTCCAGGGACCTCTCTC  
 CAACCGCTGAGGATGCTGAGCTTCTGACTTGTAGGAATGTGAGGAGACGGGAGAGCTTTGAGGAGCCTGCC  
 CCCAGGCCCCACGGGCCCCCTGCCCTGCACACGGTGTATTCGCTATCAGGCAGGGCTGAGGATG  
 AGCTGACAATCACGGAGGGTAGTGGCTGGAGGTATAGAGGAGGGAGATGCTGACCAATGGGTCAGGCTCGGA  
 ACCAGCACGGCAGGGTAGGCTTGTGAGCGATATCTCAACTTCCCGACCTCTCCCTCCAGAGAACGCC  
 AACAGACTGACAATCCCTGCGGGCAGAGCCCACAGCATTCTGCACAGGGCTCTACAGCTACACCGGACAGA  
 GTGCAGAGGAGCTGAGCTTCCCTGAGGGGCACTCATCGCTGCCCCGGGCAAGATGGAGTAGATGACG  
 GCTTCTGGAGGGGAGAAATTGGGGCCGTGTGGGGCTTCCCTGCTGGTGGAGAGCTGCTGGCCCC  
 CAGGGCCACCTGAACACTCTGACCCCTGAACAGATGCTGCGTCCCCCTCTCCTCCAGCTTCTCCCACCTGCAC  
 CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGCTGCCTGGGACAAAGCCCTGGACCTCCCTGGGTCTGG  
 ACATGATGGCACCTGACTCAGGCCATGCTCCACCCTCCCCGGCTAAAGCCCCGGATCCTGGCCACC  
 CAGATCCCCTCACCTGAAGGCCAGGAAGCCTGACCCCCAGTGTGCTGCTGCCATCTCAAGCTGTCAGA  
 CCACACCATCAATGATCCAGAGCAACACAGCAAAGCTGAATGCCCTATTCCACCCCTCACCTCAAGGGT  
 GGAAACTTGGCCCTTCCATTCTAGAGCTGGAACCCACTCTTTTCTCCATTGTTCTATCATCTAGGACC  
 GGAACACTAACCTCTCTCTGACCCATCTAGGGTGTGAAATGCCCTGAATCTGGGCTGGAAACC  
 ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTCCCCACCTGGCTCCATGACCCACCCACTCTGGATG  
 CCAGGGTCACTGGGGTTGGGCTGGGAGAGGAACAGGCTGGGAATCAGGAGCTGGAGGCCAGGATGCGAAGCAG  
 CTGTAATGGTCTGAGCGGATTATTGACAATAAAGGGCACGAAGGCCAGGGCTGGGCTTGGGCTTGG  
 CTAAGAGGGCAGGGGGCTACGGTGTATTGCTTGGGGCCACACGGGAGGGGGCTGGGCTTGGGCTTGG  
 GCTCTATCATATGGAGCGAGGTGTGGGGAGGGGGCAGGCTGAGACTGTCACCTGGGAGTGGAGCTGG  
 AGCTGGGGGCTGTGACCTCTCTGAGGCCCTCAGGCTGAGACTGTCACCTGGGAGTGGAGCTGG  
 AGCTGGGGGAGGGGGCTGTGCTGCCAGTGGAGGGGGCTTACGCCACCCACCCCTGGGCTTGGGCTTGG  
 TCCATCAGCACAATGAAGGAGACTGGAGAAGAGGAAGATAAACACTGTTGCTTCTGTCAAGCTGTG  
 TCCAG  
 TTTCCCTGGGCTCAGGACCTCCCTACCTCCACCACAAACCAAGGGATTATAGCAAAGGCTAACCTGC  
 AGTTTACTCTGGGGGTTAGGGAGCGAAAGGCTTAAATAGTTAAGTAGGTGATGGGAAGAGTAGGATTACCTCA  
 TTAGGGCTCAGGCAGACTCACCTCACACTCTCCCTGCTCCCTGTGGTAGAGAGACACCTGAGAGAAAGGGGG  
 TCAACAATGAGAGACCCAGGGAGTAGGTCTGATCAGTGCCTTGGGAGGGGGCTGGGCTTGGGCTTCAAGTG  
 AGTCCCCGGCTGTTTCTACCTGGTGTAGAAGTGTCTGGTTGCTGGCTGCCATTGCTTGG  
 GCAGGCCCTGGGCTTGGGGCTTCCCTCCGGGCTCAGTGTGGCTCTGCAGAAGCTGCTGGGGTCCCTCAAGTG  
 CACGAGGGGTAGGCTGCTGCTCCCTGAGTCTCTGAGTACTGGGGCTGGCTAGGACCTGGGGCTGGGCC  
 TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCCTGGGCTGCCCTGGGAGGCCACCCCTGACCACCCCTG  
 GGTCTGTCCCCCACCAGAGCCCCAGCTCTGTGTGGGGAGGCCATCACGGTGTCTGCTGGAGCTCCATAGCGCT  
 TCTCAATGTGTGTCACCCGGAACCTGGAGGGAGGGAACACTGGGGTTAGGACCAACTCAGAGGCTGCTT  
 GCCCTCCCTCTGACCAGGGACATCCTGAGTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGAGGCCCTC  
 AGATTGTGGGCACATTGTGAGCTGACTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGGCCAAGGCCACTT  
 TTGGGATCAGGTGCTGATCACTGGGCCCCCTACCTCAGCCCCCTTCCCTGGAGCACCTGCCACCTGCC  
 CAGAGAACACAGTGGCTCCCTGTCGGGGGGCTTTCTCTGGAGCGCTGCCAGCGACAAGTGGAG  
 GCCTCTTGCTGCGGCTGCAATGGATGCAAGGGCTGAGGCCAGGGACTGTGTGATGATGGAGGGGCTC  
 CGTCTGCAAGGTGGAGGTGGCATCCACACTGGACAGCAGGAGGGAGTGAGGGTAACATTCCATT  
 TCATGTTTGTCTTACGTTCTCAGCATGCTCTTAAACCCAGAAGCCCCAATTCCCAAGCCCCATT  
 TTCTGTCTTATCTAATAAACTCAATATTAAG

353/615

**FIGURE 350**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pi: 4.53, NX(S/T): 0
MQLAKYQSHSKCPTVFPPPTPVLCLPNQVLQRLEQRROQASEREAPSIEQRLOEVRESIRRAQ
VSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAEELSDF
EECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTTGEWEVIEEGDADEWVKA
RNQHGEVGFVPERYLNFPDLSLPESSQDSNDNPCGAEPTAFLAQALYSYTGQSAEELSPEGAL
IRLLPRAQDGVDGFWRGEFFGRVGVPSSLVEELLGPPPELSDPEQMLPSPSPPSFSPPA
PTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPAAKAPDPGHPDPLT
```

354/615

**FIGURE 351A**

CACAGGGAGACCCACAGACACATATGCACAGAGAGAGACAGAGGGAGAAAGAGACAGAGACAAAGGCACAGCGGAA  
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCAGACAGAGTCTACAGAGGGAGAGGCCAGAGAACGCTGCAGA  
AGACACAGGCAGGGAGAGACAAGAGATCCAGGAAGGGCTCAGGAGGAGAGTTGGAGAAGGCCAGACCCCTGG  
GCACCTCTCCAAGGCCAAGGACTAAGTTTCTCATTCTTAAACGGTCTCAGCCCTCTGAAAACATTGCCC  
TCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTCCAAGAGCTAGGGTGTGGAGGACTTGGT  
GCCCTAGACGGCCTCAGTCCCTCCAGTCAGTACAGTGCCTAGCAGTACAGTGCCTAGTCCCAGACAGGCTCGCATCCGGGAGGG  
CTTGGCAGGGCGCTGGCTGTGGGAGGCCAACCTGCCTCTGCTCCTCCATGTGCGCCTCTCCTGGCTGGTGTG  
GCTGCTCTGCTACTGCTGGCCTCTCCTGCCTCAGGCCGGCTGGCAGGCCCTCCCCCCTGGGAGGAGAGAT  
CGTGTTCAGAGAGCTCAACGGCAGCGCTCTGGCTCTGGCTCGGCCCTGGGAGGAGCTGGCAGGGCTGACAGTGCAGTA  
GCCCTTGGGAGAGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCGAGGAGCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC  
CCTGGGAGCAGGCGCTGAGCTGTGGGTGGAGCAGGCCCTGACAGTGGCACCATCAATGGAGATCC  
GGAGTCGGTGGCATTCTGCACGGGATGGGGAGGCCCTGTTAGGCGTGTACAATATCGGGGGCTGAACTCC  
CCTCCAGCCCCCTGGAGGGAGGACCCCTAAGTCTGCTGGGGACTGGGCTCACATCTACGCCGAAGAGTCC  
TGCCAGCGGTCAAGGTCCATGTCAACGTCAGGCTCCTTGAAGGCCAGGCCAGGCCAGAGGCCAA  
GCGCTTGCTTCACTGAGTAGATTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCGCATTCCACGGTGC  
GGGGCTAAAGCGTACCTGCTAACAGTGTAGGGCAGCAGCCAGGCCAACGCCAAGCATTCCGAATCC  
TGTCAGCTTGGTGGTACTCGCTAGTGTACCTGGGTCAGGCAGGGGCCAACAGTGGGCCAGTGTGC  
CCAGACCCTGCGCAGCTCTGTGCTGGCAGCGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACCTTGA  
CACAGCCATTCTGTTACCGTCAGGACCTGTGTGGAGTCTTCACTTGCGACACGCTGGTATGGCTGATGTGG  
CACCGTCTGTGACCAGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGCTCAGTCAGCCTTCACTGCTGCTCA  
TGAACGGGTCTATGCTTCAACATGCTTCAAGCAGCCATGCACTAGTTGAATGGCCTTGGAGCAC  
CTCTCGGCACTGTCACTGGGCTGTGATGGCTCATGGGATCTGGAGGCCCTGGTCCCCCTGAGTCCCCGCT  
CATCACTGACTTCTGGACAATGGCTATGGCAGTGTCTTCAAGACAAACAGAGGCTCATTGCACTGCGCT  
GACTTCTGGCAAGGACTATGATGCTGACCGCCAGTGCAGCTGACCTTGGGCCAGTCAAGCCATTGTCC  
ACAGCTGCCGCCCTGTGCTGCCCTGGTGTCTGGCACCTCAATGGCAGTGCCTGGCCAGACCAAACA  
CTCGCCCTGGGCCAGTGGCACACCCCTGCGGGGCCACAGGCCCTGCACTGGTGGTGTGCTGCCACATGGACCA  
GCTCCAGGACTTCAATATTCCACAGGCTGGCTGGGCTCTGGGACCATGGGTGACTGCTCTGGACCTG  
TGGGGTGGTGTCCAGTTCTCTCCGAGACTGCACAGGCCCTGCCCCCGAATGGTGGCAAGTACTGTGAGGG  
CCGCGTACCGCTTCCGCTCTGCAACACTGAGGACTGCCAACCTGGCTAGCCCTGACCTTCCGGAGGAGCA  
GTGTGCTGCCATAACCACCGCACCGACCTCTCAAGAGCTCCAGGGCCATGGACTGGTTCTCGCTACAC  
AGGCGTGGCCCCCAGGACCACTGCAAACACTCACCTGCCAGGCCGGCACTGGCTACTACTATGTGCTGGAGCC  
ACGGGTGGTAGATGGACCCCTGTTCCCGGACAGCTCTCGGTCTGTGCTCCAGGCCAGTCATCATCTGCTGG  
CTGTGATCGCATATTGGCTTCAAGAAGAAGTTGACAAGTGCATGGTGTGCGGAGGGACGGTTCTGGTGTGAG  
CAAGCAGTCAGGCTCTTCAAGGAAATTAGGTGACCGATAACAACTGTTGACTATCCCCGGGGGCCACCA  
CATTCTGTCCGGCAGGAAACCCCTGGCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCTTA  
TGGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGGTACTGCCCTGGGCACTGAGCTTGCCTA  
CAGCGGGGCACTGCAACACTGAGGACACTGTCAGGCCATGGCCACTGCCCTTGACACTGCAAGTCT  
AGTGGCTGGCAACCCCCAGGACACACGCCCTGGGATACAGCTTCTCGTGGCCGGCGACCCCTTCAACGCCAC  
CCCCACTCCCCAGGACTGGCTGACCGAAGAGCACAGATTCTGGAGATCTTGGCCGGCGCCCTGGCGGGAG  
GAAA**TAA**CTCACTATCCGGCTGCCCTTCTGGGACCCGGGCCCTGGACTAGCTGGAGAAAGAGAGAGCTT  
CTGTTGCTGCCCTAGCTAAAGACTCAGTGGGAGGGGCTGTGGGCTGAGACCTGCCCTCTCTGCCCTAA  
GCCGAGGCTGGCCCTGCCCTGGTTCTGCCCTGGGAGGCCAGTGTGGTACTGGGATGAAGGGCTGACAGAC  
AGCCCTCCATCTAAACTGCCCTCTGCCCTGGGTACAGGAGGGAGGGGAAGGCAGGGAGGGCTGGGCC  
CAGTTGTTATTGTTAGTATTCACTTTATTAGCACCAGGAAGGGAGCAAGGACTAGGGTCTGGGAA  
CTGACCCCTGACCCCTCATGCCCTACCCCTGGGCTAGGAAATCCAGGGTGGTGTGATAGGTATAAGTGGTG  
TGTGTTGCTGCTGTGTGTGTGAAAGATGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTCTC  
TTCCTGAAATTATTATTGGAAAAGAGTCAGGCTAGGGTAGGGGCTTCAAGGAGGGTGGAGGATATCTTT  
TTTTTTTCTT  
GCACAACTCAGGCTCACTGCACTCTCCGCCCTCCGGGTTCAAGTGTGTTGCTTGTGAGGAGCTGGGAGTGAATG  
GGATTACAGGCTCTGCCACCGCCAGCTAAATTGTTGTTGTTGTTGGAGACAGAGTCTGCTATTGTC  
ACCAGGGCTGGAAATGATTCACTGCAACCTGCCACCTGGGTTCCAGCAATTCTCTGCCCTAGCCTC  
CGAGTAGCTGAGATTAGGCACCTACCACGCCAGGCCAGTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT  
CATGTTGCCAGGCTGGCTCGAAGCTCTGACCTTAGGTGATCCACTCGCCTCATCTCCAAAGTGTGCTGGGATT  
ACAGGGCTGAGGCCACCGTGTGCTGGCCACGCCAACTAATTGTTGTTAGGAGACAGGGTTTACCATGT  
TGGCCAGGCTGCTCTGAACCTGACCTCAGGTAATGACCTGCCCTCCAAAGTGTGCTGGGATTACAGG

355/615

**FIGURE 351B**

TGTGAGCCACCACGCCCGGTACATATTTAAATTGAATTCTACTATTTATGTGATCCTTGGAGTCAGACAG  
ATGTGGTTGCATCCTAACCTCATGTCTGAGCAATTAGATTCTCATTTGCCAATAATAACCTCCCTAGAAG  
TTTGTGAGGATTAATAATGTAATAAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAGGAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGAAA

356/615

**FIGURE 352**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492  
><subunit 1 of 1, 837 aa, 1 stop  
><MW: 90167, pi: 8.39, NX(S/T): 1  
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLASILPSARLASPLPREEEIVF  
PEKLNGSVLPGSGAPARLLCRLQAFGETLLELEQDSGVQVEGLTVQYLGQAPELLGGAEPGT  
YLTGTINGDPESVASLHWGDGGALLGVLQYRGAEHLHQLEGGTNSAGGPGAHILRRKSPASG  
QGPMCNVKAPLGSPSPRPRRAKRFASLSRFETLVVADDKMAAFHGAGLKRYLLTVMAAAAKA  
FKHPSIRNPVSLVVTRLVILGSGEEGPVGPSAQTLRSFCAWQRGLNTPEDSGPDHFDTAIL  
FTRQDLCGVSTCDTLMADVTVCDFPARSCAIVEDDGLQSAFTAHELGHVFNMLHDNSKPCI  
SLNGLPLTSRHMVAPVMAHVDPPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGK  
DYDADRCQLTFGPDSRHCPCQLPPPACAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGG  
RCLHMDQLQDFNIHQAGGWGPWGPGDCSRTCGGGVQFSRDCTRPRNNGKYCEGRRTFR  
SCNTEDCPGTSALTFREEQCAAYNHRTDLFKSFPGPMWDWPRTGVAPQDQCKLTCQARALGY  
YYVLEPRVVDGTPCSPDSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDGSGCSKQSGSFR  
KFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTLMPSPTDVVLPGA  
VSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPTPSTPRPTPQDWLH  
RRAQILEILRRRPWAGRK

**Important features of the protein:****Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 358-367

357/615

**FIGURE 353**

GCAGGAACCTGGCTCCGGCTGGCACCTGAGGAGCAGCGTGACCCCGAGGGCCCAGGGAGCTGCC  
GGCTGGCCTAGGCAGGCAGCCGACCATGCCCAGCACGGCGTGAGCTCTGGGCTTCCTGC  
TCAGCTTCTGGGCATGGTGGGCACGTTGATCACCAACCATCCTGCCGACTGGCGAGGACAG  
CGCACGTGGGCACCAACATCCTCACGGCGTGCTCCTACCTGAAAGGGCTCTGGATGGAGTGTG  
TGTGGCACAGCACAGGCATCTACCAAGTGCAGATCTACCGATCCCTGCTGGCGCTGCCCAAG  
ACCTCCAGGCTGCCCGGCCCTCATGGTCATCTCCTGCCTGCTCTGGGCATAGCCTGCGCCT  
GCGCGTCATCGGGATGAAGTGCACGCGCTGCCAACGGCACACCCGCCAAGACCACCTTG  
CCATCCTCGGCGGCACCCCTTCATCCTGGCGGCCCTGTGCATGGTGGCGCTCCTGG  
CCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGAAGTTGAGA  
TTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGTGGCACCC  
TTTGCCTGTCCTGCCAGGACGAGGCACCCCTACAGGCCCTACAGGCCCGCCAGGGCACCA  
CGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATCGGCC  
CCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTGTGAGTCCCCACAG  
CCTGCTTCCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGG  
TTCCAGCACAAAGTTACTCTGGCAATTTGTATCCAAGGAAATAATGTGAATGCGAGGA  
AATGTCTTAGAGCACAGGGACAGAGGGGAAATAAGAGGGAGGAGAAAGCTCTATACCAA  
GAATGAAAAAAATCCTGCTGTTTGTTATTTATATATATATGTTGAGTGGGTGATTG  
TAACAAGTTAATATAAGTGAATTGGAGTTGGTCAGTGGGTGGTTGTGATCCAGGAA  
TAAACCTTGCAGTGGCTGTTATGAAAAAA

358/615

**FIGURE 354**

MASTAVQLLGFLLSFLGMVGTLLTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTLFILAGLLCMVAWSWTNDVVQNPFYNPLPSGMKFEIGQALYLGFISSSSLSLIGGTLLCLSCQDEAPYR PYQAPPRATTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

359/615

**FIGURE 355**

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTCGGCAGCAGGAGGGCGGCAGCTTCTCGC  
AGGCAGGCAAGGGCGGGCGGCCAGGATCATGTCCACCACATGCCAAGTGGTGGCGTTCCTCC  
TGTCCATCCTGGGGTGGCCGGCTGCATCGCGCCACCGGGATGGACATGTGGAGCACCCAGG  
ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGA  
GGCAGAGTCAGGCTCACCAGAATGCAGGCCCTATTCACCACATCCTGGGACTTCCAGCCATGC  
TGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCCTGGTAT  
CCATCTTGCCTGAAATGCATCCGCATTGGCAGCAGTGGAGGACTCTGCCAAAGCCAACATGA  
CACTGACCTCCGGGATCATGTTCATGGTCTCAGGTCTTGTCGAATTGCTGGAGTGTCTGTG  
TTGCCAACATGCTGGTACTAACTCTGGATGTCACAGCTAACATGTACACCCGCATGGGTG  
GGATGGTGCAGACTGTTAGACAGCAGGTAACACATTGGTGCAGGCTCTGTTCTGGGCTGGT  
CTGGAGGCCTCACACTAAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGCTGGCACCAAG  
AAGAAACCAACTACAAAGCCGTTCTTATCATGCCTCAGGCCACAGTGTGCTACAAGCCTG  
GAGGCTTCAAGGCCAGCACTGGCTTGGGTCAAACACCAAAAACAAGAAGATAACGATGGAG  
GTGCCCGCACAGAGGACGAGGTACAATCTTATCCTCCAAGCACGACTATGTG**TAA**TGCTCTA  
AGACCTCTCAGCACGGGCGGAAGAAACTCCCGGAGAGCTACCCAAAAACAAGGAGATCCCA  
TCTAGATTCTCTTGCTTTGACTCACAGCTGGAAGTTAGAAAGCCTCGATTTCATCTTG  
GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCAATAAACAGCTGAG  
TTATTATGAATTAGAGGCTATAGCTCACATTCAATCCTCTATTCTTAAATATAA  
CTTCTACTCTGATGAGAGAAATGTGGTTAATCTCTCACATTGATGATCTATTCCAGCTATCCCCAAG  
AAACTTTGAAAGGAAAGAGTAGACCCAAGATGTTATTCTGCTGTTGAATTGTCTC  
CCCACCCCAACTGGCTAGTAATAAACACTTAAGTGAAGAAGCAATAAGAGAAAGATATT  
TGTAATCTCTCCAGCCATGATCTCGGTTCTACACTGTGATCTAAAGTTACCAAAACCA  
AAGTCATTTCAGTTGAGGCAACCAACCTTCTACTGCTGTTGACATCTTATTACAGC  
AACACCATCTAGGAGTTCTGAGCTCCACTGGAGTCCTCTGTGCGGGTCAGAAA  
TTGTCCTAGATGAATGAGAAAATTATTTTTAATTAAAGTCCTAAATATAGTTAAATAA  
ATAATGTTTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG  
AAGGAATGAAAAATAATTGCTTGACATTGTCTATATGGTACTTGTAAAGTCATGCTTAA  
GTACAAATCCATGAAAAGCTCACACCTGTAATCCTAGCATTGGAGGCTGAGGAGGAAGG  
ATCACTTGAGCCCAGAAGTTGAGACTAGCCTGGCAACATGGAGAAGCCCTGTCTCACAAA  
ATACAGAGAGAAAAATCAGCCAGTCATGGTGGCATACACCTGTAGTCCCAGCATTCCGGGAG  
GCTGAGGTGGAGGATCACTTGAGCCAGGGAGGTGGGCTGCAGTGAGCCATGATCACACC  
ACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAAATAATAATGGA  
ACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTAA

360/615

**FIGURE 356**

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734  
><subunit 1 of 1, 261 aa, 1 stop  
><MW: 27856, pi: 8.50, NX(S/T): 1  
MSTTCQVVAFLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTEC  
R PYFTI LGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFI  
V SGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGG  
VMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTEDEVQ  
SYP SKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

361/615

FIGURE 357

GGAAAAACTGTTCTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTCCGG  
AGTCCAGCTGGCTAAACTCATCCCAGAGGATAATGGCACCCATGCCTTAGAAATCGCTGGG  
CTGTTCTGGTGGTGGAAATGGTGGCACAGTGGCTGTCAGTGCATGCCTCAGTGAGA  
GTGTCGGCCTTCATTGAAAACAACATCGTGGTTTGAAAACCTCTGGGAAGGACTGTGGATG  
AATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGAAAATCTATGATTCCCTGCTGGCTCTT  
TCTCCGGACCTACAGGCAGGCCAGGACTGATGTGCTGCTCCGTGATGTCCTTGGCT  
TTCATGATGCCATCCTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAAGGTGAAG  
GCTCACATCTGCTGACGGCTGGAATCATCTTCATCATCACGGCATGGTGGTGCATCCCT  
GTGAGCTGGTTGCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAATGTTGCCAA  
AAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCA CGGCACTGGTGCTGATTGTTGGA  
GGAGCTCTGTTCTGCTGCGTTTGTTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA  
CCTTCCCACATCGCACAAACCAAAAAAGTATCACACCGGAAAGAAGTCACCGAGCGTCACTCC  
AGAAGTCAGTATGTGTAGTTGTATGTTTTTAACTTACTATAAGCCATGCAAATGACA  
AAAATCTATATTACTTCTCAAATGGACCCAAAGAAACCTTGATTACTGTTCTTAACG  
CTAATCTTAAATTACAGGAACTGTGCATCAGCTATTATGATTCTATAAGCTATTCA  
TGAGATATTAACCCAATGCTTGATTGTTCTAGAAAGTATAGTAATTGTTCTAAGGTGG  
TTCAAGCATCTACTTTTATCATTACTTCAAATGACATTGCTAAAGACTGCATTATTT  
ACTACTGTAATTCTCCACGACATAGCATTATGTACATAGATGAGTGTAACATTTATCTCA  
CATAGAGACATGCTTATGGTTTATTAAAATGAAATGCCAGTCATTACACTGAATAAAAT  
AGAACTCAACTATTGCTTTCAGGGAATCATGGATAGGGTTGAAGAAGGTTACTATTAAATTG  
TTAAAAACAGCTAGGGATTAATGTCCTCATTATAATGAAGATTAAGGCTTAA  
TCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTGTTTAGCCTAGGAGTTAGAA  
ATCCTAACCTCTTATCCTCTCCAGAGGTTTTTCTTGTGTATTAATTAACATT  
TTAAGCAGATATTTGTCAGGGCTTGCATTCAAACGTTGCTTTCCAGGGCTATACTC  
AGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTGGTTAGGAAAGTGAAGGCTTAA  
GTTTTGTATTTGAAGAAGAATGATGCAATTGACAAGAAATCATATATGTATGGATATATT  
TAATAAGTATTTGAGTACAGACTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAATAT  
GTCTGGTTTCATTGCTTACAAAAAAACAACAACAAAAAGTTGTCCTTGAGAACTTC  
ACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTGTTCTGTGAAAATAAATTTC  
CTCTTGTAACCATTCTGTTAGTTACTAAAATCTGAAATACTGTATTTCTGTTATT  
CCAAATTGATGAAACTGACAATCCAATTGAAAGTTGTGCGACGTCTGTAGCTAAAT  
GAATGTGTTCTATTGCTTATACATTATTAATAATTGTACATTCTAATT

362/615

**FIGURE 358**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735  
><subunit 1 of 1, 225 aa, 1 stop  
><MW: 24845, pi: 9.07, NX(S/T): 0  
MATHALEIAGLFLGGVGMVGTAVTVMPOWRVSAFIENNIVFENFWEGLWMNCVRQANIRMQ  
CKIYDSLLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGIIF  
IITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCN  
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

363/615

**FIGURE 359**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTGCCCTCTGCTCGCGCCCC  
GGCGCAATGGCTGCCTCCCCCGCGGCCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGCTC  
CTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTAAAAA  
CGAGAAGCACCTGTCCAACTAAGACTAAAGTGGCCGTTGATGAGAATAAGCAAAGAACATT  
CTTGGCAGCCTGAAGGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCGAGGTGCAGCAG  
TGGTACCAGCAGTTCTCATGGGCTTGATGAAGCGAAATTGAAGATGACATCACCTAT  
TGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCACTATGAT  
GAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTAGGCATGGAGCCAGCGTCAACTAC  
GATGACTACTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCTCTCATGT  
ATCTCCTAATGCCTTACACTACTTGGTTCTGATTGCTCTATTCAAGCAGATCTTCTACC  
TACTTTGTGTGATAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTTGATATTCAAT  
GGAAATGCCTCTCATTTAAAATAGAAATAAAGCATTGGTAAAAAGA

364/615

**FIGURE 360**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742  
><subunit 1 of 1, 148 aa, 1 stop  
><MW: 17183, pI: 8.77, NX(S/T): 0  
MAASPARPAVLALTGLALLLLCWGP GG ISGNKLKMLQKREAPVPTKTVAVDENKAKEFLG  
SLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNRDRNGHEY YGDYYQRHYDED  
SAIGPRSPYGFRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

365/615

FIGURE 361

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAGA  
TTCCCCAGGCCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCCTAACGAAACCATCAGGCCCTC  
AGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTGGTCAGCAGCTTT  
CTTGCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCAGGTGCTGCAGCTGGAG  
GACTTGGATGGGTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTGTGGAAAGC  
AAGTTCAACATATCAAAGATAAAATGAAAATGCGGATGGAAGCTTGACTATGGCCTCTCCAG  
ATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAACCTTGCCACGTAGAC  
TGTCAAGATCTGCTGAATCCAACCTTCTTGCAGGCATCCACTGCGAAAAAGGATTGTGTCC  
GGAGCACGGGGATGAACAACGGTAGAATGGAGGTTGCAGTGTCAAGGCCGGCCACTCTCC  
TACTGGCTGACAGGATGCCGCTGAGATGAAACAGGGTGCAGGTGCACCGTGGAGTCATTCCA  
AGACTCCTGCTCACTCAGGGATTCTCATTCTTCTTCTACTGCCTCCACTTCATGTTAT  
TTTCTTCCCTCCATTACAACAAAATGACCAGAGCCCCAGGAATAAATGGTTTCTTGG  
CTTCCTCCTTACTCCCCTGGACCCAGTCCCTGGTTCTGTCTGTTATTGTAAACTGAGG  
ACCACAATAAAGAAATCTTATATTATCG

366/615

**FIGURE 362**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746  
><subunit 1 of 1, 148 aa, 1 stop  
><MW: 16896, pI: 6.05, NX(S/T): 1  
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKIN  
ENADGSFDYGLFQINSHYWCNDYKSYSSENLCVDCQDILLNPNLLAGIHCAKRIVSGARGMNNW  
VEWRLHCSGRPLSYWLTCRLLR

**Signal peptide:**

amino acids 1-18

367/615

**FIGURE 363**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCA~~G~~CCCTGCTTGACTGAGAACCCAC  
CAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGAAAGAAACACCTGAGCA  
GAATGGAATCATTATTTTCCCAAGGAGAAACCGGGTAAAGGGAGGGAAAGCAATTCAAT  
TTGAAGTCCCTGTGAATGGGCTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGGACTTGG  
GGTGAACCTGGGTCTGTGGTTCTGATTGTAAGTGGAAAGCAGGTCTTGACACCGCTGTG  
GCAAATGTCAGGACCAGGTTAAGTGA~~T~~CTGGCAGAAAAACTTCAGGTTGAA~~C~~AAGCAACCCAT  
GTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTA~~A~~CTGAACATGACCTGTTGC  
ATTGGCAGTTCTAGCAACATGCTCTTAAGGAAGCGATA~~C~~AGGCACAGACC~~A~~TCAGACTCC  
AGTTCCCTCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGC~~G~~ATGTTGCACCCCTC  
CCCACACACCCTGCACCAGACTGT~~C~~ACAGCCCAAGCCAGCAAGCACAGCC~~C~~CTGAAGCCAGGT  
ACCGCCTGGACTTGGGAATCCCAGGATTGGTACTGGAAAGCTGAGGATGAGGGTGAAGAGT  
ACAGCCCTCTGGAGGGC~~T~~GCCACCC~~T~~TATCTCACTGCGGGAGGATCAGCTGCTGGTGGCCG  
TGGCCTTACCCCAGGCCAGAAGGAACCAGAGCCAGGGAGGGAGGTTGGAGCTACCGCCTCA  
TCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGGGCTGATGAGGACG  
GGGAGGTGTCTGAAGAAGAGGAGTTGACCCGTCAGCCTGGACCCACGTGGCCTCCAGGAGG  
CACTCAGTGC~~CC~~GCATCCCCCTCCAGAGGGCTCTGCCAGGCCAGCGTCATCCTCTGTTCCATGATGAGGACCT  
AGCAGCACCC~~T~~CAGGACAGCCTGCCACAGCCAGCGTCATCCTCTGTTCCATGATGAGGACCT  
GGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGCCAGGGC~~T~~TC~~T~~GAAGG  
AGATCATCCTCGTGGAC~~C~~CTCAGCCAGCAAGGACA~~A~~CTCAAGTCTGCTCTCAGCGAATATG  
TGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAGGCTGGTGCCTCATGGATGCCACTAGGGGCC  
GGATGCTGGGGGCCACCAGAGCCACCAGGGGATGTGCTCGTCTCATGGATGCCACTGCGAGT  
GCCACCCAGGCTGGCTGGAG~~CC~~CTCCTCAGCAGAATAGCTGGTACAGGAGGCCAGTGGTAT  
CTCCGGT~~G~~ATAGATGTGATTGACTGGAAAGACTTCCAGTATTACCCCTCAAAGGAC~~T~~GCAGC  
GTGGGGTGTGGACTGGAA~~G~~CTGGATTCCACTGGAAC~~C~~TTGCCAGAGCATGTGAGGAAGG  
CCCTCCAGTCCCCATAAGCCCCATCAGGAGCC~~T~~GTGGTGC~~CC~~GGAGAGGTGGTGGCCATGG  
ACAGACATTACTTCAAAACACTGGAGCGTATGACTCTCTTATGTC~~G~~CTGCCAGGTGGT~~G~~AAA  
ACCTCGA~~A~~CTGTCTTCAAGGCC~~T~~GGCTCTGTGGCTCTGTTGAA~~A~~ATCCTCC~~T~~GC~~T~~TC  
GGTAGGACACATCTACAAAATCAGGATTCCATTCCCCCTCGACCAGGAGGCCACCC~~T~~GA  
GGAACAGGGTCGCATTGCTGAGAC~~T~~GGCTGGGT~~C~~ATTCAAAGAAAC~~T~~TCTACAAGCATA  
GCCAGAGGCC~~T~~TC~~C~~CTTGAGCAAGGCTGAGAAGCCAGACTGCATGGAA~~G~~C~~T~~GCAGCTGC  
AAAGGAGACTGGGTGT~~C~~GGACATTCCACTGGTTCTGGCTAATGTC~~T~~ACCC~~T~~GAGCTGT~~A~~CC  
CATCTGAACCCAGGCCAGTTCTGTGGAAAGCTCCACAAACACTGGACTTGGCTCTG~~C~~AG  
ACTGCCAGGCAGAAGGGACATCCTGGCTGT~~C~~CCATGGTGTGGCT~~C~~TTGCA~~G~~TCAG~~C~~AGGCC  
GGCAGCAACAGTAC~~T~~GCAGCACACCAGCAGGAAGGAGATTC~~A~~CTTGGCAGCCACAGCACC  
TGTGCTTGCTGT~~C~~AGGCAGGAGCAGGTGATTCTTCAGAA~~A~~CTGCACGGAGGAAGGCC~~T~~GGCCA  
TCCACCAGCAGC~~A~~CTGGACTTCAGGAGAATGGGATGATTGTC~~C~~ACATTCTTCTGGAAAT  
GCATGGAAAGCTGTGT~~C~~AGGAAAGAA~~A~~ATAAAGATTGTACCTGGCT~~C~~GTGATGGAAAAG  
CCCGCCAGCAGTGGCGATTGACCAGATAATGCTGTGGATGAACGAT~~TGA~~ATGTC~~A~~ATGTCAG  
AAGGAAAAGAGAA~~T~~TTGGCCATCAA~~A~~ATCCAGCTCCAAGTGAACG~~T~~AAAGAGCTTATATATT  
TCATGAAGCTGATC~~T~~TTGTGTGCTC~~T~~TTGTGTTAGGAGAGAAAAAGCT~~T~~ATGAAA  
GAATATAGGAAGTTCTC~~T~~TTTACACCTTATTGACTGCTGGCTGCTTA

368/615

**FIGURE 364**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pi: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLMLGCVIMMVAMLHPPHTLHQTVTAQASKHSPEARYRLDFGE
SQDWVLEAEDEGEYEYSPLEGPPFISIREDQLLVAALPQARRNQSQGRGGSYRLIKQPRRQ
DKEAPKRDWGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHPQDS
LPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIILVDDLSQQGQLKSALSEYVARLEGV
KLLRSNKRLGAIRARMLGATRATGDVLFMDAHCECHPGWLEPLLSRIAGDRSRVVSPVIDVI
DWKTFQYYPSKDLQRGVLDWKLDHFWEPLPEHVRKALQSPIRSPVPGEVVAMDRHYFQN
TGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATLRNRVRIA
ETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRILGCRTFHFLANVYPELYPSEPRPS
FSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSPQHLCFAVRQ
EQVILQNCTEEGLAIHQHQHWDFOENGIVHILSGKCMEAVVQENNKDLYLRPCDGKARQQWRF
DQINAVDER
```

**Signal peptide:**

amino acids 1-28

369/615

FIGURE 365

GGAGAGAGGCGCGCGGGTGAAAGGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGCG  
AGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCCTGCCCGC  
AGCCGGAGCCATGCGACCCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCTCCTGC  
TGCTCCTGCTGCTGCAGCTGCCCGCCGTCAGCGCCTCTGAGATCCCCAAGGGGAAGCAAA  
AGGCGCAGCTCCGGCAGAGGGAGGTGGACCTGTATAATGGAATGTGCTTACAAGGCCAG  
CAGGAGTGCCTGGTCAGACGGAGCCCTGGGCCAATGTTATTCCGGGTACACCTGGATCC  
CAGGTGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTGAGGAGTCCT  
GGACACCCAACTACAAGCAGTGTTCATGGAGTTCAATTGGCATAGATCTTGGAAAAA  
TTGCGGAGTGTACATTACAAAGATGCGTCAAATAGTGCCTAAGAGTTGTCAGTGGCT  
CACTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTCACATTCAATGGAGCTG  
AATGTTCAAGGACCTCTCCCATTGAAGCTATAATTATTGGACCAAGGAAGCCCTGAAATGA  
ATTCAACAATTAAATTACATCGCACTCTCTGTGGAAGGACTTGTGAAGGAATTGGTGT  
GATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTA  
CTGGATGGAATTCACTGTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTAATT  
CATTGCTACCTTTTTTATTATGCCTGGAATGGTCACTTAAATGACATTAAATAAG  
TTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTACAGACCAAGTGTGATTCA  
CACTGTTTAAATCTAGCATTATTGCTTCAATCAAAGTGGTTCAATATT  
TAGTTGGTTAGAATACTTCTCATAGTCACATTCTCAACCTATAATTGGAATATTGTT  
TGGTCTTTGTTCTTAGTATAGCATTAAAAAAATATAAAAGCTACCAATCTTG  
TACAATTGTAAATGTTAAGAATTTTTATATCTGTTAAATAAAATTATTCCAACA

370/615

**FIGURE 366**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVP
GRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAEC
TFTKMRNSNSALRVLFGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTI
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

371/615

**FIGURE 367**

GTAAACCAGCGCAGTCCTCCGTGCGTCCGCCGCCGCTGCCCTCACTCCC GCCAGG**ATGGC**  
ATCCTGTCCTGGCCCTGCGCATGGCGCTGCTGGTCTCCGGGTTCTGGCCCTGCGGTGCT  
CACAGACGATGTTCCACAGGAGCCGTGCCCACGCTGTGGAACGAGCCGGAGCTGCCGTC  
GGGAGAAGGCCCGTGGAGAGCACCAGCCCCGGCCGGAGCCCGTGGACACCGGTCCCCCAGC  
CCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGC GGCTGGACCAGGGCGGCG  
GTCGCTGGGCCCGCTATCGCGGCATCGTGATGCCGCCCTGCTGGCACCTGCGTGGT  
GCTGGCGCTCGTGGTCGTCGGCTGAGAAAGTTTCTGCCCTC**TGA**AGCGAATAAAGGGCCG  
CGCCCGGCCGCGGCGACTCGGCAAAAAAAAAAAAAA

372/615

**FIGURE 368**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398  
><subunit 1 of 1, 121 aa, 1 stop  
><MW: 12073, pI: 4.11, NX(S/T): 0  
MASCLAIRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTGP  
PAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

373/615

**FIGURE 369**

GGCCGTTGGTTGGTGC CGCGGCTGAAGGGTGTGGCGCAGCAGCGTCGGTGGTTGGCCGGCGGC  
GGGCCGGGACGGGCATGCCCTGCTGCTGCTGCCTGGTGCCTGACGGCGCGCTGGCCCACG  
GCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTAACT  
TCAAGTCTGGTGGTGGCGACATCCCCGTGTCAGGGCGCTGCTACCGACTGGAGCGACG  
ACACGATGAAGGAGCTGCACCTGCCATCCCCGCAAGATCACCCGGAGAAGCTGGACCAAG  
TGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGAGAGATGTACTTCCCCGGT  
ATTTCCCAACGAGCTGCACAAACATCTCCGGAGCAGGTGCACCTCATCCAGAACGCCATCA  
TCGAAAGGCACCTGGCACCAAGGCAGCTGGGGAGGGAGGGCAGCTCTCCAGGGAGGGACCCAGCC  
TAGCACCTGAAGGATCAATGCCATACCCCGCGGGGACCTCCCCTAAGTAGCCCCAGAGGCG  
CTGGGAGTGTGCCACCGCCCTCCCCGTAAAGTTGCTCCATCTCACGCTGGGGTCAACCTGG  
GGACCCCTTCCCTCCGGGCATGGACACACATACATGAAAACCAGGCCATCGACTGTCAGC  
ACCGCTGTGGCATCTCCAGTACGAGACCATCTCTGCAACAACACTGCACAGACTCGCACGTG  
CCTGCTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGTGCCAGGGCCCTAC  
TGTCCCTGGGTCCCAGGCTCTCTGGAGGGGCTCCCCGCCTCACCTGGCTGTCACTCGG  
GTAGGGCGGGGCCGTGGGTTCAAGGGCGCACCACCTCCAAGCCTGTCCTCACAGGTCTCGG  
CGCAGTGAAGTCAGCTGTCCAGGGCCTCTGAACTACATAAAACTGGCACAAGTAAGTCC  
CCTCCTCAAACCAACACAGGCACTGTGTGTAGTGAGCACCTCGTGGGTGAGTATGTGGGG  
CACAGGCTGGCTCCCTCAGCTCCACGCTCTAGAGGGGCTCCCGAGGAGGTGGAACCTCAACC  
CAGCTCTGCGCAGGAGGCGGTGCACTCCTTCTCCCTCAAAGGTCTCCGACCCCTCAGCTGG  
AGGCAGGCATCTTCTAAAGGGTCCCCATAGGGTCTGGTCCACCCATCCCAGGTCTGTGG  
TCAGAGCCTGGGAGGGTCCCTACGATGGTTAGGGGTGCCCATGGAGGGCTGACTGCCCA  
CATTGCCCTTCAGACAGGACACGAGCATGAGGTAAGGCCGCCCCGACCTGGACTTCAGGGGA  
GGGGGTAAAGGGAGAGAGGGAGGGCTAGGGGCTCTAGATCAGTGGGGCACTGCAAGGT  
GGGGCTCTCCCTATACCTGGACACCTGCTGGATGTCACCTCTGCAACCACACCATGTGGT  
GTTTCATGAACAGACACCACGCTCCTCTGCCCTCTCCCTGGGACACACAGAGGCCACCCGG  
CCTTGTGAGTGACCCAGAGAAGGGAGGGCTGGGAGAAGGGTGTGCTGTAAGCCAACACCAGC  
GTGCCGCGGCTGCAACCCCTCGGACATCCCAGGCACGAGGGTGTGCTGGATGTGGCCACAC  
ATAGGACACACGCTCCAGCTGGAGGGAGAGGCCTGGGCCCCCAGGGAGGGAGGCAGGGGT  
GGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCCCGCAGCCTGGTATGCCAGCCTTAAGGT  
GTCTGGAGCCCCACACTTGGCCAACCTGACCTTGGAAAGATGCTGCTGAGTGCTCAAGCAGC  
ACTGACAGCAGCTGGCCTGCCAGGGCAACGTGGGGGGAGGAGACTCAGCTGGACAGCCCT  
GCCTGTCACTCTGGAGCTGGCTGCTGCCTCAGGACCCCTCTCCGACCCGGACAGAGC  
TGAGCTGCCAGGGCAGGGAGGGAGGGAGGGAAATGGGGTGGGCTGTGCGCAGCATCAG  
CGCCTGGCAGGTCCGCAAGAGCTGCGGGATGTGATTAAAGTCCCTGATGTTCTC

374/615

**FIGURE 370**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399  
><subunit 1 of 1, 157 aa, 1 stop  
><MW: 17681, pI: 7.65, NX(S/T): 1  
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMKE  
LHLAI PAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNI FREQVHLIQNAIIERHL  
APGSWGGQQLSREGPSLAPEGSMPSPRGDLP

**Signal peptide:**

amino acids 1-15

375/615

**FIGURE 371**

CCGGGCTGTGCAGAGACGCC**ATGT**TACCGGCTCCTGTCAAGCAGTGACTGCCCGGGCTGCCGCC  
CCGGGGCTTGGCCTCAAGCTGCGGACGACGCCGGTCCATCAGCGGCCGGCTGCCGCCTC  
TCGGCCACGGCTGGGTGCCCCGGCTCGGGCTGGGCTGGGCTCGGGTGAAGCTGG  
CAGGTGGGCTGAGGGGCGCGCCACAGGGAGCAGTCCCCCGCGGCCCGACCCCTGAGGCCTGC  
CTCTGGCCGAGGCCACAGGGAGCAGTCCCTGCCCGTGGTCTCCGAGACCCCAGGCC  
CCTGCTCAGGTGCTCGCCAGAGCCATCGAGAGCAGCCGCACCTGCTGCACAGGATCAAGG  
ATGAGGTGGCGCACGGGCATAGTGGTTGGAGTTCTGTAGATGAAAAGAAGTCTGGTCAG  
AAGGTTAGGTTATGCTGATGTTGAGAACCGTGACCATGTAACACAGAGACAGTTATGCGAA  
TTGCTAGCATCAGCAAAGTCTACCATGGTTGCTCTGCCAAATTGTGGGAAGCAGGGAAAC  
TGGATCTGATATTCCAGTACAACATTATGTTCCGAATTCCCAGAAAAAGAATATGAAGGTG  
AAAAGGTTCTGTACAACAAGATTACTGATTTCCATTAAAGTGGAAATCGTCATTATGAAA  
AGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAACGCTTGAAGATGATGAAAGAGAATG  
TTGCATTGAGCAAGAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTACTAAATTAAAA  
CAGAGCAGGAGAATGAAGCCAATGCCGAATTCAAAACCTGGCAAGAAAAAGAATGATTTG  
AACAAAGGCAATTATATTGAGAGAAAAGTGTGAAAATTCAATTGAATCCCTAAGATTATTTA  
AAAATGATCCTTGTCTTCAAACCTGGTAGTCAGTTTGATTCAACTTTGGCTATACCC  
TAATGGCAGCCATAGTAGAGAGAGCTCAGGATGTAAATTGGACTATATGCAGAAAATAT  
TCCATGACTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGCCAGTGATTACAATAGAG  
CAAGG**TAA**ATGAATACTTCTGCTGTCTAGCTATATGCCATCTAACACTATTTATTAAT  
TAAAAGTCAAATTCTTGTGTTCCATTCCAAAATCAACCTGCCACATTGGAGCTTTCT  
ACATGTCATCTGTTCTCATCTGAAAGTGAAGGAAGTAAAACATGTTATAAAGTAAAAAA

376/615

**FIGURE 372**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522  
><subunit 1 of 1, 373 aa, 1 stop  
><MW: 41221, pi: 8.54, NX(S/T): 0  
MYRLLSAVTARAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLALGVKLAGGLRGA  
APAQSPAAPDPEASPLAEPPEQSLAPWSPQTAPPSCRCFARAIESSRDLLHRIKDEVGAPG  
IVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLSLTVALAKLWEAGKLDLDIPV  
QHYVPEFPEKEYEGEKGVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAFEQEK  
EGKSNEKNDFTKFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESLRLFKNPLFF  
KPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTQEEENEPVIYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

377/615

**FIGURE 373**

GAATACGGGGAGAGAGAGGAGACCAGGACAGCTGCTGAGACCTCTAAGAACGATACTAA  
GAGCAAAGATGTTCAAACTGGGGCCTCATGTCTTCTACGGCTGTTAGCCCAGACCATGG  
CCAGTTGGAGGCCTGCCGTGCCCTGGACCAGACCTGCCCTGAATGTGAATCCAGCCCTG  
CCCTTGAGTCCCACAGGTCTGCAGGAAGCTTGACAAATGCCCTCAGCAATGCCGTGCT  
GGGGCCTGTTGGCATTCTGGAAAACCTCCGCTCCTGGACATCCTGAAGCCTGGAGGAGGT  
ACTTCTGGTGGCCTCCTGGGGACTGCTTGAAAAGTGACGTCAGTGATTCCCTGGCCTGAAC  
AACATCATTGACATAAGGTCACTGACCCCCAGCTGCTGGAACCTGGCCTGTGCAGAGCCCT  
GATGCCACCGTCTATGTCACCATCCCTCGGCATAAGCTCCAAGTGAATACGCCCTG  
GTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTAGCTGTG  
AGAGATAAGCAGGAGAGGATCCACCTGGCCTTGGTACTGCACCCATTCCCTGGAAGCCTG  
CAAATTCTCTGCTTGATGGACTTGGCCCCCTCCCCATTCAAGGTCTCTGGACAGCCTCACA  
GGGATCTGAATAAGTCCTGCCTGAGTTGGTCAAGGCAACGTGTGCCCTCTGGTCAATGAG  
GTTCTCAGAGGCTTGGACATCACCCTGGTCATGACATTGTTAACATGCTGATCCACGGACTA  
CAGTTGTCATCAAGGTCTAAGCCTTCCAGGAAGGGCTGGCCTCTGCTGAGCTGCTTCCAG  
TGCTCACAGATGGCTGGCCATGTGCTGGAAGATGACACAGTTGCCTCTCCGAGGAACCT  
GCCCTCTCCTTCCCACCAGCGTGTAAACATCCATGTGCCTCACCTAATAAAATGGCT  
CTTCTTATGCA

378/615

**FIGURE 374**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76533
><subunit 1 of 1, 256 aa, 1 stop
><MW: 26713, pI: 5.62, NX(S/T): 0
MFQTGGLIVFYGLILAQTMAQFGGLPVPLDQTLPLNVNPALPLSPTLAGSLTNALSNGLL
SGGLLGILENLPLL DILKPGGGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGL
VQSPDGHRLYVTIPLGIKLQVNTPLVGASLLRILAVKLDITAEILAVRDKQERIHLVLGDC
THSPGSLQISLLDGLGPLPIQGLLDSLTGILNKVLPELVQGNVCPLVNEVRGQDITLVH
DIVNMLIHGLQFVIKV
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-19

**Transmembrane domain:**

Amino acids 79-97

**N-myristoylation sites:**

Amino acids 46-52; 49-55; 58-64; 62-68; 66-72; 80-86; 81-87;
82-88; 85-91; 86-92; 89-95; 202-208; 233-239

379/615

**FIGURE 375**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCCTT  
AAATATGTCAAGATCCAGACTTTCACTGGTCACCTCAGCGATCTCAACGATAAGGGATCTGTG  
TTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCAGCGAAGAAGATGAAATGTGTG  
TTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTGGTGGC  
AGCTCTCTCTGTGGAGCTGTGGCCTCTGCCCTCCAGTGCTGGCTGAGGAGACCCGAATTGA  
TTCTCACAGGCGCACCATGGCAGTTTGCTGTGGAGACTGGACTCTATTATGGACAGA  
AGCAGCTGTGAGTCCAACGTGGAAATCACCTCAAACCTCAAACCCCTGACCTATATCCTGT  
TCCTGCTCCATGTTGGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGAAAAACAAAC  
CTGATTTAGGTGTGGATTATCAATTAAAGTATTAACGACATCTGTAATTCCAAAACATCAA  
ATTAGGAATAGTTATTCAGTTGGAAATGTCCAGAGATCTATTCAATAGTCTGAGGAA  
GGACAATTGACAAAAGAATGGATGTTGGAAAAATTGGTATGGAGATGTTAAATAGTA  
AAGTAGCAGGCTTGATGTGTCAGTGCTGTATCATACTTTATGCTACACAACCAAATTAAAT  
GCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTTCCATCACATTAA  
GGACTCCACTGCAGTATACAGCACACCATTGCTTTAAACTCTTCCTAGCATGGGTCC  
ATAAAAATTATTATAATTAAACAATGCCAAGCCGAGAATCCAACATGTCCAGAACAGAAC  
CAGAAAGATAGTATTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAGAAAAGTTGGAGTTG  
AAGGGTAAAGGATAATGAAGAGGAAAAGGAAAGATTACAAGTCTCAGCAAAACAAAGAGGT  
TTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGAAGGAGATTGCTGAAGATA  
TAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTCCCCTTTACAGTAATGAATGT  
GGCCTCCATAGTCCATAGTGTGTTCTCTGGAGCCTCAGGGCTTGGCATTATTGCAGCATCATG  
CTAAGAACCTCGGCATAGGTATCTGTTCCATGAGGACTGCAGAAGTAGCAATGAGACATCT  
TCAAGTGGCATTGGCAGTGGCCATCAGCAGGGGACAGACAAAAACATCCATCACAGATGA  
CATATGATCTCAGCTGACAAATTGTTGAACAAAACAATAACATCAATAGATATCTAAAAA

380/615

**FIGURE 376**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, PI: 4.99, NX(S/T): 0
MSRSRLFSVTSAI STIGILCLPLFQLVLSLPCEEDEMCVNNDQHPNGWYIWILLLVAA
LLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPPTVGIHLQTQTPDLYPVP
APCFGPLGSPPPYEEIVKTT
```

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

381/615

FIGURE 377

CGCGGGATCGGACCCAAAGCAGGTGGCGGCAGGCAGGAGAGCAGGCCGGCGTCAGCTCCTCG  
ACCCCCGTGTCGGGCTAGTCAGCGAGGCAGGGCGGCAGGGCCATGGCCAGGCCGGC  
ATGGAGCGGTGGCGCACCGCTGGCGCTGGTGAACGGGGCCTCGGGGGCATCGGCGCGGC  
GTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGCTGCAGGCCACTGTGGCAAC  
ATCGAGGAGCTGGCTGCTGAATGTAAGAGTCAGGCTACCCGGACTTTGATCCCCTACAGA  
TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC  
GGTGTAGACATCTGCATCAACAATGCTGGCTTGCCCCGGCTGACACCCTGCTCTCAGGCAGC  
ACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGCCCTCAGCATCTGCACACGGGAA  
GCCTACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGACATCATTAACATCAATAGCATG  
TCTGGCCACCGAGTGTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC  
ACTGCCTGACAGAGGGACTGAGGCAAGAGCTCGGGAGGCCAGACCCACATCCGAGGCCACG  
TGCATCTCTCCAGGTGTGGAGACACAATTGCCCTCAAACCTCCACGACAAGGACCTGAG  
AAGGCAGCTGCCACCTATGAGCAAATGAAGTGTCTCAAACCGAGGATGTGGCGAGGCTGT  
ATCTACGTCTCAGCACCCCCGACACATCCAGATTGGAGACATCCAGATGAGGCCACGGGAG  
CAGGTGACCTAGTGAUTGTGGAGCTCCTCTCCCTCCCCACCCCTCATGGCTTGCCCTCTG  
CCTCTGGATTTAGGTGTTGATTCTGGATCACGGGATACCAACTTCTGTCCACACCCCGACC  
AGGGGCTAGAAATTGTTGAGATTTATATCATCTTGTCAAATGCTTCAGTTGTAATG  
TGAAAAATGGGCTGGGAAAGGAGGTGGTGTCCCTAATTGTTTACTTGTAACTTGTCTTG  
TGCCCCCTGGGCACTGGCCTTGTCTGCTCTCAGTGTCTCCCTTGACATGGGAAAGGAGTT  
GTGGCCAAAATCCCCATCTCTGACACTAACGTCTGTGGCTCAGGGCTGGGCTGGCAGAGG  
GAGGCCTTCACCTTATATCTGTGTTATCCAGGGCTCCAGACTTCCCTCTGCCTGCC  
ACTGCACCCCTCTCCCCCTTATCTATCTCCTCTGGCTCCCCAGCCAGTCTGGCTTGT  
CCCCCTCTGGGCTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCTGGC  
CCAGTGGATTCATGGTGATCATTAAAAAGAAAAATCGCAACCAAAAAAAAAAAA

382/615

**FIGURE 378**

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCARTVGNIEELAAECKSAGYPGT  
LIPYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNLALS  
ICTREAYQSMKERNVDDGHIININNSMSGHRLPLSVTHFYSATKYAVTALTEGLRQELREAQT  
HIRATCISPGVvetQFAFKLHDKDPEKAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ  
MRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

383/615

FIGURE 379

GAGCGGAGTAAAATCTCCACAAGCTGGAACAAACCTCGTCCAACTCCCACCCACC GGCGT TCTCCAGCTCGATCTGGAGGCTGCCAGTGTGGGACGCAGCTGACGCCGCTATTAGC TCTCGCTGCCTGCCCGGCTCAGAAGCTCCGTCGGCGGCCGACCGTGACGAGAAGGCCACG GCCAGCTCAGTTCTCTACTTTGGAGAGAGAGAAAGTCAGATGCCCTTAAACTCCCT CTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATAACAACCTTGCTGAAGATGAA GAATATAACAATTGAGGATATTTTTCTTTCAAGTCTGATTGTGGCTTACACT CAAGTTACCATTTCAAGTCTGTTGCTTCTTCAGAAATGTTTACAATCTC AAGAAAAAATATGCCCAGAAATTGAGTTACTGTTGCTGTATTGGACTCATTGGGGATT GATGTTACTGCACTATACTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTTACGTGAGCA AATACTAGACTTAAGAAAAGATATGTTAAAGCTCTAGCAGAGGAAATAAGAACACAGTGG A TGTCGAGAACGGTGCCTCTATGGCAGGATATGCGGATCTGAAAAGAACAAATTGCTGTCCTTCT GGATGACATTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATATTGTTGTAATGG CTCAGCAGCCAACACCAACCAATGGTACTAGTGGAAATTGGTGCCTAGTAACCACAAATAAAAG AACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGCTGCTCCATCCACTG TGGATTATATCCTATGGCAGAAAAGCTTATAATTGCTGCTTAGGACAGAGCAATACTTTAC AATAAAAGCTCTACACATTTCAAGGAGTATGCTGGATTCTGAACTCTAATTCTGTACATA AAAATTAAAGTTATTGTTGCTTCAGGCAAGTCTGTTCAATGCTGTACTATGCTTAA AGAGAATTGGTAACTGGTGTGGTAAGCAGATAGGTGAGTTTGATAAAATCTTTGT GTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTCTTCTATAACACATTAT TTAAGTATATAACACGTTTTGGACAAGTGAAGAATGTTAATCATCTGTCATTGTTCTC AATAGATGTAACGTGTTAGACTACGGCTATTGAAAAAATGTGCTTATTGTACTATTTGTT ATTCCAATTATGAGCAGAGAAAGGAAATAATGTTGAAAATAATGTTGAAATCATGACCC AAAGAAATGTATTGATTGACTATCCTCAGAATAACTGAAGGTTAATTATTGTATTTTA AAAATTACACTTATAAGAGTATAATCTGAAATGGTAGCAGCCACTGTCCATTACCTATCGT AAACATTGGGCAATTAAACAGCATTAAAATAGTTGAAACTCTAATCTTATACTTATTG AAGAATAAAAGATATTTATGATGAGAGTAACAATAAGTATTCTGATTTTCACATACAT GAATGTTCTATTAAAGTTAATCCTTGAGTGTCTATGCTATCAGAAAGCACATTATTCC ATATTGGGTTAATTGCTTTATTATATTGGCTTAGGAGGAAGGGACTTGGAGAATGGAA CTCTGAGGACTTAGCCAGGTGTATATAAAAGTACTTTGTGCTGCATTAAATTGCTTG GAAAGTGTAAACATTATATTATAAGAGTATCCTTATGAAATTGTAATTGTATAACAGA TGCATTAGATATTCTATTATATAATGCCACTAAAATAAGAACATTAAAATATAACTAT GAAGATTGACTATCTTCAGGAAAAAGCTGTATATAGCACAGGAAACCCTAATCTGGGTA ATTCTAGTATAAAACAAATTATACTTTATTAAATTCCCTGTAGCAAATCTAATTGCCAC ATGGTGCCTATATTCTAGTATTCTCTATAGTAACGTCTTAAGTGCAGCTAGCTTCT AGATTAGACTATAGAATTAGATATTGTATTGTTCGTCATTATAATATGCTACCACATGT AGCAATAATTACAATATTATTAAATAATGTGAAATATTGTTCATGAAAGACAGATT TCCAAATCTCTCTCTCTGTACTGTACCTTATGTGAAGAAATTAAATTATATGCCA TTGCCAGGT

384/615

**FIGURE 380**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648  
><subunit 1 of 1, 140 aa, 1 stop  
><MW: 15668, pI: 10.14, NX(S/T): 5  
MFFTISRKNMSQKLSLLLLVFGLIWGLMLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE  
NKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNLVP  
VTTNKRTNVSGSIR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

385/615

**FIGURE 381**

AACTTCTACATGGGCCTCCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACC  
ATCATGCCCTCCCACCCCTCTTGACTGCGGGCGTTCAAGGTGCAGAGTCTCAGTTGCCCGG  
GAGCACCTCCCCCTCCGAGGCAGTCTGCTCAGAGGGCTCGGCCAGAATTCCAGTTCTGGTT  
TCATGCCAGCCTGTAAAAGGCCATGGAACCTTGGGTGAATCACCGATGCCATTAAAGAGGGTT  
TTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTTCTGCCGTGTTCAAGTAGGCCACCAG  
CCACCTGTGGCGTTGAGTGCTGAAATGAGGAACTGAGAAAATTAAATTCTCATGTATTTT  
CTCATTATTTATTAAATTAACTGATAGTTGATCATATTGGGGGTACATGTGATATTGG  
ATACATGTATAACAATATAATGATCAAATCAGGGTAACGGGATATCCATCACATCAAACAT  
TTATTTTATTCTTTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGC  
ATCTCAGCTTACTGCAACCTCTGCCAGGTCAAGCGATTCTCATGCCCTCACCTCCAA  
GTAGCTGGGACTACAGGCATGCACCACAATGCCAACTAATTGTTGATTAGAGACG  
GGGTTTGCCATGTTGCCAGGCTGGCCTGAACCTCTGCCCTCAAACAATCCACTGCCCTCG  
GCCCTCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAAACATTATCTTT  
CTTGTTGGAACTTGAAATTACAATGAATTATTGTTAAGTGCATCTCCCTGCTGTG  
CTATGGAACACTGGGACTTCTCCCTCTATCTAACCTCTGATCACCTCATTCTACTCTACCTC  
ACTTCATCCCCACTCCTCTCTATCCTCCAACCTCTGATCACCTCATTCTACTCTACCTC  
CATGAGATCCACTTTTAGCTCCACATGTGAGTAAGAAAATGCAATATTGTTCTGCTG  
CCTGGCTTATTCACTTAACATAATGACTTCTGTTCCATGTTGCTGCAAATGACAGGA  
TTTCGTTCTTAATTCAATTAAAATAACCACACATGGCAAAA

386/615

**FIGURE 382**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSSRGSLLRGPRPRIPVLVSCQ  
PVKGHGTLGESPMFKRVFCQDGTVRSFCVCAVFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

387/615

**FIGURE 383**

TTCTGAAGTAACGGAAGCTACCTGTATAAAGACCTCAACACTGCTGACC**ATGATCAGCGCAG**  
CCTGGAGCATCTCCTCATCGGGACTAAAATTGGGCTGTTCCCTCAAGTAGCACCTCTATCAG  
TTATGGCTAAATCCTGTCCATCTGTGTGCGTGCATCGGGTTCTACCTGTAATGATC  
GCTTTCTGACATCCATTCCAACAGGAATACCAACAGGATGCTACAACCTCTACCTTCAGAACAA  
ACCAAATAATAATGCTGGGATTCCCTCAGATTGAAAAACTGCTGAAAGTAGAAAGAATAT  
ACCTATACCAACACAGTTAGATGAATTCCCTACCAACCTCCAAAGTATGTAAGAGAGTTAC  
ATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTCAAAATTCCCTATCTGG  
AAGAATTACATTAGATGACAACACTCTGCTCTGCAGTTAGCATAGAACAGGGAGCATTCCGAG  
ACAGCAACTATCTCGACTGCTTTCTGTCCCCTAATCACCTTAGCACAATTCCCTGGGTT  
TGCCCAGGACTATAGAAGAACTACGCTGGATGATAATCGCATATCCACTATTCATCACCAT  
CTCTTCAGGTCTCACTAGTCTAAAACGCCCTGGTTCTAGATGAAACCTGTTGAACAATCATG  
GTTTAGGTGACAAAGTTCTTCAACCTAGTTAATTGACAGAGCTGCTCCCTGGTGCAGGAATT  
CCCTGACTGCTGCACCAAGTAACCTCCAGGCACAAACCTGAGGAAGCTTATCTCAAGATA  
ACCACATCAATCGGGTGCACCAATGCTTTCTTATCTAAGGCAGCTATGACTGGATA  
TGTCCAATAATAACCTAAGTAATTACCTCAGGGTATCTTGATGATTGGACAATATAACAC  
AACTGATTCTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGT  
TACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAAAGGTTTC  
GTGGGATGGCTATTAAGGACTCAATGCAAGACTGTTGATTGTAAGGACAGTGGATTGAA  
GCACCAATTCAAGATAACCACGTCAACACAGTGTATCCTGCCAAGGACAGTGGCCAG  
CTCCAGTGACCAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG  
GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTCACCTCTGATACCATTCATA  
TCTCTGGAAACTTGCTCTACCTATGACTGCTTGAGACTCAGCTGGCTTAAACTGGGCATA  
GCCCGGCATTGGATCTATAACAGAAACAATTGTAACAGGGGAACGCAGTGAGTACTGGTCA  
CAGCCCTGGAGCCTGATTCACCCCTATAAAAGTATGCATGGTCCCATGGAAACCAAGCAACCTCT  
ACCTATTGATGAAACTCCTGTTGATTGAGACTGAAACTGCACCCCTCGAATGTACAACC  
CTACAACCAACCTCAATCGAGAGCAAGAGAAAGAACCTACAAAACCCCAATTACCTTGG  
CTGCCATCATTGGTGGGCTGTGGCCCTGGTTACCATGCCCTTCTGCTTACTGTGTTGGT  
ATGTTCATAGGAATGGATCGCTCTCAAGGAACGTGCACTATAGCAAAGGGAGGAGAAGAA  
AGGATGACTATGCAAGACTGGCACTAAGAACGACAACCTATCCTGGAAATCAGGGAAACTT  
CTTTCAAGATGTTACCAATAAGCAATGAACCCATCTCGAAGGAGGAGTTGTAATACACACCA  
TATTTCTCTTAATGGAATGAATCTGTACAAAACAATCACAGTGAAGCAGTAGTAACCGAA  
GCTACAGAGACAGTGGTATTCCAGACTCAGATCACTCACACT**TGATGCTGAAGGACTCACA**  
GCAGACTTGTGTTGGTTAAACCTAAGGGAGGTGATGGT

388/615

**FIGURE 384**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCNDRFLTSIPTGI PEDA TTL  
YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNL PKYVKE LHLQENNIRTITYDSLSK  
IPYLEELHLD DNSVSAVSIEEGAFRDSNYLRLFLSRNHILSTIPWGLPRTIEELRLDDNRIST  
ISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKL  
YLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPGIFDDLDNITQLILRNPNWYCGCKMKW  
VRDWLQSLPVKVNVRGMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQ  
GQWPAPVTKQPDIKNPKLKDQQTGSPSRKTITITVKS VTS DTI HISWKLALPM TALRLS WL  
KLGHSPA FGSITETIVTGERSE YLVTALEPDSPYKVC M VPMETSNLYLFDETPVC IETET APL  
RMYNPTT TLNREQEKEPYKNPNLPLAAIIGGAVALVTI ALLALVCWYVHRNGSLFSRNCAYS K  
GRRRKDDYAEAGTKKD NSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNL YKNNHSES  
SSNRSYRD SGIPDSDHS HS

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,

640-645

**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44

389/615

**FIGURE 385**

CCGTCATCCCCCTGCAGCCACCCCTCAGAGTCCTTGCCCAGGCCACCCAGGCTTCTGG  
CAGCCCTGCCGGGCACCTGTCTTCATGTCTGCCAGGGGAGGTGGGAAGGAGGTGGGAGGAG  
GGCGTGAGAGGCAGTCTGGGCTGGGCAGAGCTCAGGGTGTGAGCGTGTGACCAGCAGTGA  
GCAGAGGCCGGCATGCCAGCCTGGGCTGCTGCTCCTGCTTACTGACAGCACTGCCACC  
GCTGTGGTCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCT  
GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTAGAACAGAGGCTGCCTGAAATCACCT  
GGATGGCATGGTGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAGTGTCCGGAGAAGTGGC  
CCAGGAGCCCCCTGCTGCAGCCGCTGAGCCTGCGCTGGGGATGCTGGGGAGAAGCTGGAGG  
TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCAAAGTACCTAACAGAGATTCCA  
GCTGACCCCTCCAGCCCCGGTTTGGAAAGCTCCACATGCCTGGATCCACACTGATGCCCTCCT  
GGTGTACCCCACGTTGGGCCCCAGGACTCATTCTCAGAGGAGAGAAGTGAACGTGTGCCCTGGT  
GCAGCTGCTGGGAACCGGGACGGACAGCAGCAGCAGCCCTGCGGCCTCTCAGACCTCTGAGGAG  
CCTCATGACCAAGCCCCGGCTGCTCAGGCTACTGCCTGTCCCACCAACTGCTCTTCTCCTG  
GCCAGAAATGAGGGATGCACACAGGACCACTCCAACAGAGCCAGGACTATATCACCTCTT  
CTGCGCCAACATGATGGACTGAAACCGCAGAGCTGAGGCATGGATAACGCCTACCCCTACCCG  
GGACATCTCATGGAAAACATCATGTTCTGGAATGGCGGCTCTCCGACTTCTACAAGCT  
CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAACAGCAGGAAGGATGCTGGGGAGCCTGA  
TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTCGAGGAGAGTGAA  
GAGGCAGAAAAACAATTCCAGATTCTCGCTGTTGCTCAGGCTGGAGTACAGTGGCGCAA  
TCTCGGCTCACTGCAACCTTGCCTCTGGGTTCAAGCAATTCTCTGCCTCATCCTCCGAG  
TAGCTGGGACTACAGGAGCGTGCACCCATACCTGGCTAATTTTATATTTTTAGTAGAGAC  
AGGGTTTACATGTTGCTCATGCTGGTCTCGAACCTCTGATCTCAAGAGATCCGCCACCTC  
AGGCTCCCAAAGTGTGGATTATAGGTGAGGCCACCGTGTGGCTGAAAAGCACTTCAAA  
GAGACTGTGTTGAATAAGGCCAAGGTTCTGCCACCCAGCACTCATGGGGCTCTCTCCCC  
TAGATGGCTGCTCCTCCCACACACAGGCCACAGCAGCTGGCAGCCCTGGGTGGCTTCCCTATACA  
TCCCTGGCAGAACACCCCCCAGCAAACAGAGAGGCCACCCATCCACACCGCCACCAAGCA  
GCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGAACAGACCCCTTAGTCCTCA  
TCCCTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAA  
GCCACCCGACACCAATCTTGGAAAGCCCTGAGTAGGCAGGGCAGGGTAGGTGGGGCCGGG  
AGGGACCCAGGTGTGAACGGATGAATAAGTTCAACTGCAACTGAACTGAAAAAA

390/615

**FIGURE 386**

MSARGRWEGGGRRACRGSILGLARAQGAERVTSSEQRPMASLGLLLLLTLAPPLWSSSLPG  
LDTAESKATIADLILSALERATVFLERQLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPL  
SLRVGMLGEKLEAAIQRSLLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQ  
DSFSEERSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQ  
GPLQQSQDYINLFCANMMDLNRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS  
WQKQQEGCFGEPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSQLQPLP  
PGFKQFSCLILPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

391/615

**FIGURE 387**

GGTCTGAGTCAGAGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTCCGTCTGCTGC  
TGCTGCTGCTATCGGGGATGTCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGG  
GAGGGAGTGGGGTCCGCATAGGAGATCGCTCAAGATTGAGGGCGTCAGTTGTTCCAGGGG  
TGAAGCCTCAGGACTGGATCTCGCGGGCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTT  
TCCTTAAGACAGATGGAGTTTGTGGTCATGATATAACCTCTGGATCTTATGTAGTGBAAG  
TTGTATCTCCAGCTACAGATTGATCCCCTGAGTGGATATCATTGAAAGGAAAATGA  
GAGCAAGATATGTGAATTACATCAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAA  
TGAAATCTCAGGTCACCTTACTTTATTAAAAGGGATCGTGGGCTGGACAGACTTC  
TAATGAACCCAATGGTTATGATGATGGTTCTCCTTATTGATATTGTGCTTCTGCCTAAAG  
TGGTCAACACAAGTGATCCTGACATGAGACGGAAATGGAGCAGTCATGAATATGCTGAATT  
CCAACCATGAGTTGCCGTGATGTTCTGAGTTCATGACAAGACTCTCTCTTCAAAATCATCTG  
GCAAATCTAGCAGCGGCAGCAGTAAACAGGCAAAAGTGGGCTGGCAAAAGGAGGTAGTCAG  
GCCGTCCAGAGCTGGCATTCGACAAACACGGCAACACTGGGTGGCATCCAAGTCTGGAAAAA  
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCGACGTTGATCTTACAACGTGTATGTT  
AACTTTTAGCACATGTTGACTTGAGTACCGAGAAAACCCAGCTTCATCTTGCTGT  
ATGAGGTCAATATTGATGTCAGTGAATTAAATTACAGTGTCTATAGAAAATGCCATTAATAAAA  
TTATATGAACTACTATACATTATGTATTTAATTAAACATCTTAATCCAGAAATCAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAA

392/615

**FIGURE 388**

MAAALWGFFPVLLLLLSDVQSEVPGAAAEGSGGSGVGIGDRFKIEGRAVPGVKPQDWIS  
AARVLVDGEEHVGFLKTDGSFVVHDIPGSYVVEVSPAYRFDPVRVDITSKGKMRARYVNYI  
KTSEVVRLPYPLQMKGSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPPLLIFVLLPKVVNTSDPD  
MRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSGSSKTGKGAGKRR

**Important features of the protein:**

**Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

393/615

**FIGURE 389**

GTCGTGTGCTTGGAGGAAGCGCGGAACCCCCAGCGTCCATGCGTGGAGCCTGGAG  
CTGGCTGGGTGGCTGCCTGCTGGTGTCAAGCATTGGAATGGTACCACTCCGAAATGTCAG  
AATGAATTCTGTTAATTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTGCCAAAGGGAA  
CCTGACTTTCACAGCTCAGTACCTAAGTTAGGATATTCAAGATAATGCATGAATACTAC  
CTTGACGGAATGTGATTCTCAAGTCTTCCAAGTATGGGACCACTTGAGAGTCAGGGC  
TGAATTGAGATGAGCATTCAAGACTGGTAACATCACCTCTGCTGTGGATGACACCAT  
TATTGGACCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTACATATGCCTTCTAGC  
CCCTAAAATTGAGAATGAATACGAAACTGGACTATGAAGAATGTGTATAACTCATGGACTTA  
TAATGTGCAATACTGGAAAACGGTACTGATGAAAAGTTCAAATTACTCCCCAGTATGACTT  
TGAGGTCCCTCAGAAACCTGGAGCCATGGACAACCTATTGTTCAAGTTCGAGGGTTCTTCC  
TGATCGGAACAAAGCTGGGAATGGAGTGAGCCTGTGTGAGCAAACAAACCATGACGAAAC  
GGTCCCCTCCTGGATGGTGGCGTCATCCTCATGGCCTCGGTCTTCATGGTCTGCCTGGCACT  
CCTCGGCTGCTCTCCTTGCTGTTACAAGAAGACAAAGTACGCCCTCTCCCTAG  
GAATTCTCTCCACAGCACCTGAAAGAGTTTGGGCCATCCTCATCATAACACACTTCTGTT  
TTTCTCCTTCCATGTCGGATGAGAATGATGTTGACAAGCTAAGTGTATTGAGAAGA  
CTCTGAGAGCGGCAAGCAGAACACTGGCTGGGCACAGTGACGTACTCCATCTC  
ACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAAGGGCAAGACCATCTGAGCCAGCCCCA  
CATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACATTAAAGGCTGTCTGGCA  
AAAATACTCCATTGGAACTCACTGCCATTATAAAGGTTCATGATGTTTCAGAAGTTGGC  
CACTGAGAGTGTAAATTTCAGCCTTATATCCTAAATAAGATCATGTTAATTGAGA  
AACAGGGCCGAGCACAGTGGCTCACGCCGTAAATACCAGCACCTAGAGGTGAGGCAGGG  
ATCACTTGAGGTAGGAGTTCAAGACCGCCTGCCAATATGGTAAACCCAGTCTACTAA  
AAATACAAAAATTAGCTAGGCATGATGGCGCATGCCATAATCCAGCTACTCGAGTGCCTGA  
GGCAGGAGAATTGCATGAACCCGGAGGGAGGAGGAGGAGGTTGCAGTGAGCCGAGATAGCGGC  
ACTGCACTCCAGCCTGGGTGACAAGTGAGACTCCATCTCAAAAAAAAAAAATTGTG  
AGAAACAGAAATACCTAAAATGAGGAATAAGAATGGAGATGTTACATCTGGTAGATGAAACAT  
TCTACCAGATTATGGATGGACTGATCTGAAATCGACCTCAACTCAAGGGTGGTCAGCTCAAT  
GCTACACAGAGCACGGACTTTGGATTCTTGCACTTGAATTTATTCTACCTATAT  
ATGTTTATATGCTGCTGGTGCATCAAAGTTTACTCTGTGTTGC

394/615

**FIGURE 390**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551  
><subunit 1 of 1, 325 aa, 1 stop  
><MW: 37011, pi: 5.09, NX(S/T): 4  
MAWSLGSWLGCGLLVSALGMVPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQ  
DKCMNTTILTECDFSSL SKYGDHTLRVRAEFADEHSDWVNITFCPVDDTIIGPPGMQVEVLADS  
LHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKGNTDEKFQITPQYDFEVLRNLEPWTTYCV  
QVRGFLPDRNKAGEWSEPVCEQTTHDETVPSSVMAVILMASVFMVCLALLGCFSLWCVYKKT  
KYAFSPRNSLPQHLKEFLGHPHHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNP GDSCSL  
GTPPGQGPQS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 222-245

**N-glycosylation sites.**

amino acids 49-53, 68-72, 102-106, 161-165

**N-myristoylation sites.**

amino acids 6-12, 316-322

395/615

**FIGURE 391**

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGCCAAGGTTCTGACGCG**ATG**AGGA  
AGCACCTGAGCTGGTGGCTGCCACTGTCTGCATGCTGCTCTCAGCCACCTCTGC  
TCCAGACGAGGGCATCAAGCACAGAACATCAAGTGAACCGGAAGGCCCTGCCAGCAGC  
AGATCACTGAGGCCAGGTGGCTGAGAACCGCCCCGGAGCCTTCATCAAGCAAGGCC  
TCGACATTGACTTCGGAGCCAGGGCACAGGTACTACGAGGCCACTACTGGCAGTTCCC  
ATGGCATTCCACTACAACGGCTGCTTGAGGCTAATGTGACCAAGGAGGCATTGTCACC  
GCATCAATGCCACCCAGCGCGAACCAAGGGAGTCCAGAACAGCAGACAACAAGCT  
AGCAGGTGCTCTGGCGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTGG  
AGAGGGCGCAGGACTTCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTCTGG  
TCTGGCTCATGGTAAA**TAA**GCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCGAG  
TCCTGGCAAGTGAACCAGCTTCTCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGC  
GGCGATGCACTCGCAATGCCGCTCCCACGTATGCGCCCTGGTATGTCCTGCGTTCT  
GATAGATGGGGACTGTGGCTTCTCCGTCACTCATTCTAGCCCTAGCAGAGCGTCTGG  
CACTAGATTAGTAGTAAATGCTTGATGAGAACACATCAGGCAGTGCCACCTGCTTC  
AGTACTTCCAACAACTCTTAGAGGTAGGTGTATTCCCGTTTACAGATAAGGAAACTGAG  
CCAGAGAGCTGAAGTACTGCACCCAGCATCACCAGCTAGAAAGTGGCAGAGCAGGATT  
CCTGGCTTGTCTAACCCCCAGGTTCTGCTCTGCCAATTCCAGAGCTGTGGTGTACT  
TATGTCTCACAGGGACCCACATCCAAACATGTATCTTAATGAAATTGTGAAAGCT  
TAGAAATAATGAAAACACACTGA

396/615

**FIGURE 392**

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWRKALPSTAQITEAQVAENRPGAFIKQG  
RKLDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNK  
LHQQLWRLVQELCSLKHFCEFWLERGAGLRVTMHQPVLLCLLALIWLVMVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

397/615

**FIGURE 393**

TGAAATGACTTCCACGGCTGGGACGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA  
TGGTGAAGGTGCCTGTCTAACTTTCTGTAAAAAGAACCGAGCTGCCTCCAGGCAGCCAGCCCT  
CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGGAGCTGCTTCGCCAA  
TTAACACCAAGAAGAATTGAGGCTGCTGGGAGGAAGGCCAGGAGGAACACGAGACTGAGAG  
**ATGA**ATTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTCTGCCCTCTTTG  
CTGGCGACAGCCTCTCAAATGCAGATGGTGTGCTCCCTGCCTGGGTTTACCCCTGCTTCTC  
TGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACCTTGGGCCCTGCCAAGTGAAGGGG  
GTTGTTCCCCAGAAACTGTGAGGAAAGCCTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGAT  
AACATCAGAGTGCCCAGGCTGCTGCAGCAGGAGGTCTGCAGAACGTCTCGGATGCTGAGAGC  
TGTTACCTGTCCACACCCCTGCTGGAGTTCTACTTGAAAAGTGTGTTCAAAAACCACCAAAAT  
AGAACAGTGAAGTCAGGACTCTGAAGTCATTCTACTCTGGCCAACAACATTGTTCTCATC  
GTGTCACAACGTGCAACCCAGTCAAGAAAATGAGATGTTCCATCAGAGACAGTGCACACAGG  
CGGTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAACAGCTGACCAAAGCC  
CTTGGGAAAGTGGACATTCTCTGACCTGGATGCAGAAATTCTACAAGCT**TGA**ATGTCTAGA  
CCAGGACCTCCCTCCCCCTGGCACTGGTTGTTCCCTGTGTCATTCAAACAGTCTCCCTTCC  
TATGCTGTCACTGGACACTTCACGCCCTGGCATGGTCCCATTCTGGCCAGGATTATT  
GTCAAAGAAGTCATTCTTAAGCAGCGCCAGTGCAGTCAGGGAGGTGCCTCTGGATGCTGT  
GAAGAGTCTACAGAGAAGATTCTGTATTATTACAACCTATTTAATTAAATGTCACTATTTC  
AACTGAAGTTCTATTATTGTGAGACTGTAAGTTACATGAAGGCAGCAGAACATTGTGCC  
ATGCTTCTTACCCCTCACAACTCCTGCCACAGTGTGGGCAGTGGATGGGTGCTTAGTAAGT  
ACTTAATAAAACTGTGGTGCTTTTTGGCCTGTCTTGGATTGTTAAAAAACAGAGAGGGATG  
CTTGGATGTAACACTGAACCTCAGAGCATGAAAATCACACTGTCTCTGATATCTGCAGGGAC  
AGAGCATTGGGTGGGGTAAGGTGCATCTGTTGAAAAGTAAACGATAAAATGTGGATTAAA  
GTGCCAGCACAAAGCAGATCCTCAATAAACATTCAATTCCCACCCACTGCCAGCTCAC  
CCCATCATCCCTTCCCTGGTGCCTCCTTTTTTATCCTAGTCATTCTCCCTAATCT  
TCCACTTGAGTGTCAAGCTGACCTGCTGATGGTGACATTGCACCTGGATGTAATCAATC  
TGTGATGACATTCCCTGCTAATAAAAGACAACATAACTCCAAAAAAAAAAAAAAA  
AAAA

398/615

**FIGURE 394**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002  
><subunit 1 of 1, 206 aa, 1 stop  
><MW: 23799, pi: 9.12, NX(S/T): 3  
MNFQQRLQSLWTLARPFCPPLLATASQMOMVVLPCLGFTLLLWSQVSGAQGQEFGFGPCQVKKG  
VVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVHTLLEFYLKTVFKNHHN  
RTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRRAFKQLDVEAALTKA  
LGEVDILLTWMQKFYKL

**Signal sequence:**

amino acids 1-42

**N-glycosylation sites.**

amino acids 85-89, 99-103, 126-130

399/615

**FIGURE 395**

GCCTGGCCTCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT  
TTCCTGATTTATAGACTCAAAGAAAACTCATGTTCAGAAGCTCTTCTCTGGCCTC  
CTCTCTGTCTTCTTCCCTTTCTTATTAAATTAGTAGCATCTACTCAGAGTCATGCA  
AGCTGGAAATCTTCATTTGCTTGTCAAGTGGGTAGGTCACTGAGTCTTAGTTTATTTT  
TGAAATTCAACTTCAGATTCAAGGGGTACATGTGAAGGTTGTTATGAGTATATTGCAT  
GATGCTGAGGTTGGGT

400/615

**FIGURE 396**

MFRSSLLFWPPLCLLSLFLLLILISSIYSESCKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGT  
CEGLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68

401/615

**FIGURE 397**

**CATG**CCGCTGCCGCCGCTGCTGTTGCTCCTGGCGGCCCTGGGGACGGGCAGTCCCTG  
TGTCTCTGGTGGTTGCCTAAACCTGAAACATCACCTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGTCTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT  
CATATATGGCAAAAGAAATGGCTGAATAATCAGAACATGCAGAAATATCAATAGAACCTACTG  
TGATCTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCAAAGTTAAGGCCATTG  
GGGAACAAAGTGTCCAATGGCTGAAAGTGGACGGTTCTATCCTTTTAGAAACACAAAT  
TGGCCCACCAGAGGGTGGCACTGACTACAGATGAGAACGTCCATTCTGTTGTCCTGACAGCTCC  
AGAGAAGTGGAAAGAGAAATCAGAACACCTCCTGTTCCATGCAAACAAATATACTCCAATCT  
GAAGTATAACGTCTGTGTGAATACTAAATCAAACAGAACGTGGTCCAGTGTGACCAA  
CCACACGCTGGTGCTCACCTGGCTGGAGCGAACACTCTTACTGCGTACACGTGGAGTCCTT  
CGTCCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAACAGTGTGCCAGGACTTGAAAGA  
TCAATCATCAGAGTTCAAGGCTAAAATCATCTCTGGTATGTTGCCCATATCTATTACCGT  
GTTTCTTTCTGTGATGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA  
CCCAGCAAATTGATTTGATTTGAAATGAATTGACAAAAGATTCTTGTGCCTGCTGA  
AAAAATCGTGATTAACCTTATCACCTCAATATCTGGATGATTCTAAAATTCTCATCAGGA  
TATGAGTTACTGGGAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGGCCAGCGGGAA  
CCTGAGGCCCTCAGGAGGAAGAGGGTGAACATTAGGGTATGCTTCGCATTTGATGGA  
AATTTTTGTGACTCTGAAGAAAACACGGAAAGGTACTTCTCACCAGCAAAGACTCCCTCAG  
CAGAACAAATACCCCGATAAAACAGTCATTGAATATGAATATGATGTCAAACCAACTGACAT  
TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTGCAGGAGGAGGTGTCACACAAGGAACATT  
ATTGGAGTCGCAGGCAGCGTGGCAGTCTGGGCCGCAAACGTTACAGTACTCATACACCCC  
TCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA  
AGAGCCATCGACGACCCCTGGTCAGTGGATCCCCAAACTGGCAGGCTGTGATTCTTCGCT  
GTCCAGCTTCGACCAGGATTCAAGAGGGCTGCGAGCCTCTGAGGGGGATGGGCTGGAGAGGA  
GGGTCTTCTATCTAGACTCATGAGGAGCCGGCTCAGACAGGCCACCAGGAGAAAATGAAAC  
CTATCTCATGCAATTCAATGGAGGAATGGGGTTATATGTGCAGATGGAAAAT**TGAT**GCCAAACA  
CTTCCTTTGCCTTTGTTCCAGTTGAGTCACCCCTTGATCCCAGGCCATAAA  
GTACCTGGGATGAAAGAAGTTTCCAGTTGTCAGTGTCTGTGAGAA

402/615

**FIGURE 398**

MPLPPLLLLLLAAPWGAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYF  
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQI  
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN  
HTLVLTWLEPNLTYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV  
FLFSVMGYSIYRYIHVGKEKHPANLILIGNEFDKRFFVPAEKIVINFITLNISDDSKISHQD  
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS  
RTIPPDKTVIEYEYDVRTTDICAGPEEQELSLOEEVSTQGTLLSQAAALAVLGPQLQSYTP  
QLQDLDPLAQEHTDSEEGPEEPSTTLVDWDPQTGRLCIPSLSFDQDSEGCEPSEGDSLGE  
GLLSRLYEEPAPDRPPGENETYLMQFMEEWGLYVQMAN

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 240-260

**N-glycosylation sites.**amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,  
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

**N-myristoylation sites.**

amino acids 53-58, 106-111, 368-373, 492-497

**Tissue factor**

amino acids 1-278

403/615

**FIGURE 399**

CCGGCGATGTCGCTCGTGTGCTAAGCCTGGCCCGCTGTGCAGGAGGCCGTACCCGAGAG  
CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA  
ATCCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAACAGGGAC  
TATTCAATTGATGAATGTAAGCTGGGTACTCCGGCAGATGCCAGCATCCGTTGTAAG  
GCCACCAAGATTTGTGTGACGGGAAAAGCAACTTCCAGTCCTACAGCTGTGAGGGCAAT  
TACACAGAGGCCCTCCAGACTCAGACCAGACCCCTGGTGTAAATGGACATTTCTACATC  
GGCTTCCCTGTAGAGCTGAACACAGTCTATTCAATTGGGCCATAATATTCTTAATGCAAAT  
ATGAATGAAGATGGCCCTTCATGTCGTGAATTCACCTCACAGGCTGCCTAGACCACATA  
ATGAAATATAAAAAAAAGTGTGCAAGGCCGGAAAGCCTGTGGATCCGAACATCACTGTTGT  
AAGAAGAATGAGGAGACAGTAGAAGTGAACCTCACAAACCACTCCCTGGGAAACAGATACTG  
GCTCTTATCCAACACAGCACTATCATCGGGTTTCTCAGGTGTTGAGCCACACCAGAAGAAA  
CAAACGCGAGCTTCAGTGGTATTCCAGTGACTGGGATAGTGAAGGTGCTACGGTGCAGCTG  
ACTCCATATTTCTACTTGTGGCAGCGACTGCATCCGACATAAGGAACAGTTGTGCTCTGC  
CCACAAACAGGCGTCCCTTCCCTCTGGATAACAAACAAAAGCAAGCCGGAGGCTGGCTGCCT  
CTCCTCCTGCTGTCTGCTGGTGGCCACATGGGTGCTGGCAGGGATCTATCTAATGTGG  
AGGCACGAAAGGATCAAGAAGACTTCTTTCTACCAACCACACTACTGCCCCCCATTAGGTT  
CTTGTGGTTACCCATCTGAAATATGTTCCATCACACAATTGTTACTTCACTGAATTCTT  
CAAACCATTCAGCAGAGTGAGGTATCCTGAAAAGTGGCAGAAAAGAAAATAGCAGAGATG  
GGTCCAGTGCAGTGCTTGCCACTCAAAGAAGCAGCAGACAAAGTCGTCTCCTTCC  
AATGACGTCAACAGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAC  
TCTCAAGACCTCTCCCCCTGCCTTAACCTTCTGCAGTGATCTAAGAAGCCAGATTCT  
CTGCACAAATACGTGGTGGTCACTTAGAGAGATTGATACAAAGACGATTACAATGCTCTC  
AGTGTCTGCCCAAGTACCAACCTCATGAAGGATGCCACTGCTTCTGTGCAGAACTTCTCCAT  
GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATACAAGCCTGCCACGATGGCTGCTCCTTG  
TAG

404/615

**FIGURE 400**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTSVATGDYS  
ILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGF  
PVELNTVYFIGAHNIPNANMNEGPGMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKK  
NEETVEVNFTTPLGNRYMALIQHSTIIGFSQVFEPHQKQTRASVVIPTVGDSEGATVQLTP  
YFPTCGSDCIRHKGTVVLCPQTGVFPFLDNNSKPGGWLPLLLSLLVATWVLVAGIYLMWRH  
ERIKKTSFSTTLLPPIKVLVVYPSEICFHHTICYFTEFLQNHCRCSEVILEKWQKKKIAEMGP  
VQWLATQKAADKVVFLLSNDSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLH  
KYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201  
and 283 - 287

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-452

405/615

**FIGURE 401**

GGGAACAGGAACTATCAGCCCAGCGCTCCGGGCCCTGCATTCTCTAGCC**ATG**GACCG  
GGACCTTTGCAGTCGCTAAATTGCCACGGGCGTCTTGCTCTACTTCGGAG  
CGAACAGCAGGACAATCCACACTTCCGTAGCCTCTGGGTCGGCCGCCAGGCCCG  
GGGCCGCGCCCCAGCACCCGTTGCAGGGCAGAAAAGAGAAGAGAGTTGACAACATCGA  
GATAACAGAAATTCTCATCCTCAAAAAAGCGGATCTGCTTTGCACCTTCCTGAAATCAGA  
TGCACCTGCAACTCTGAAATTAAATGAAGACAGTGAAGATCATTATGCAATCATGCCACC  
TTTAGAGCAATTCTGAGATACCTAGTATGGATCGGAGAGAGCTGTTTCCGAGATAT  
TGAGCGTGGTGATATAGTGAATTGGAAGAATTAGTTCTATTGGAAATTGGTTTTTCAT  
GGTGTGATCTGTTAGGAAGTGGTATCATGAGAGATATAGCCCACCTAGAAATCACAGC  
TCTTGTCCCTTAAGAGATGTGCCTCTCACAGTAACCAGGGATCCTTATCATATTA  
CCAAACTGGTGACATCATTGAGCTGGAATCAAGGATATTGACAGATACCATGAAAAGCT  
AGCAGTATCTCTGTATAGCTCTCTCCACACACCTATCTGGTATTAAATTAGGTGT  
AATTAGCTCTGAAGAGCTCCTTATACTACAGGAGAAGTGGTGAAGCTAAATAGCAATT  
TTTGGAGTCTTATGAAAATGTCATGCAGAGTCTGGGATTTGTTAATCCAGGAGTAGT  
TGAATTCTCTAGAAAAACTAGGAATAGATGAATCTAATCCACCATTTAATGAGAGG  
CCTACAAAGCAAAATTCTCTGAAGATGATTTGCTCTGCATTGAGAAAAAAACAATC  
CGCATCTGGGCTTAAATGTGTGAAGATCGGAGTTGACTATTTAAAGTGGACGCCA  
TGTGGATGCTATGAATGAATAAAAGCTTGGAAATAGACAAACAAACGTGGAAGC  
TTTGGTAGCTCGTGGAGCATTATATGCACAAAGGAAGTTGAACAAAGCAATAGAAGA  
TTTGAGCTGCATTAGAAAATGTCCAATCACAGAAATGCAAGAAAATACCTCTGCCA  
GACACTTGTAGAGAGAGGAGGACAGTTAGAAGAAGAAGAAAAGTTTAAATGCTGAAAG  
TTACTATAAGAAAGCCTTGGCTTGGATGAGACTTTAAAGATGCAGAGGATGCTTGCA  
GAAACTTCATAAATATATGCAGAAATCTTGGATTAAAGAGAAAAACAAGCTGAAAAGGA  
AGAAAAGCAGAAAACAAGAAAATAGAAACAAGTGCAGAAAAGTGGCTAAGCTTAA  
AGAAGAGAAGAGGCTAAAGAAGAAAAGAAGAAAATCAACTTCTCAAGTGTGTTCTC  
TGCTGATGAATCAGTGTCTTCATCATCCTCTCTCTGGTCACAAAGGCATTCACTAGGGC  
ATCCTCAAATCAGATAGATCAGAAATAGGAAAGATGAGTGCCTACCCAGTCCAGCTAATAC  
TTCAGCATTTCTTAACCATAACAAGAAGTGGAGAAACTACTGGGAAGCAGGATAG  
GTACAGTATGAAAAGACACAGATAAAAGAGAAAGATAGATGCCCCTCTCATCTTC  
ACTTGAAATACCGGATGATTTGGAGTGTACTCTATTATTTAAAAGTTAAACTATAAA  
ACAGCCTCAGGCAGGTCTCAGGAGATATTCCAGAAGAGGGCATTGTTATCATAGATGA  
CAGCTCATTCACTGTTACTGACCCCTGAAGACCTCAAGTGGACAAGATATGGAGGTGGA  
AGACAGTGGTATTGATGATCCTGACCAAGGG**TAG**GCTTAGGTTATGTGTATGTGT  
CTAGTTTAAACAAAAATTAAAAGTAAAAAAACTAAAATAGAAAATGCTTAGAG  
AATAAGGATATAAAGAATATTGGCAGTTGAACAATGAGTGCCTAAGCTAAATGTCA  
TCACAAAAGAGTAAAAAATTACAAAATTAAAATGTTAAAGTAAAAAGCTCTAGG  
AAGCTAAGGTCAATTATTATTGGAGAAATAAAATTATTTATGAATTACTGT

406/615

**FIGURE 402**

MDRDLLRQSLNCHGSSLLSLLRSEQQDNPHFRSLLGSAAEPARGPPPQHPLQGRKEKRV  
D NIEIQKFISKKADLLFALSWKS DAPATSEINEDSEDHYAIMPPLEQFMEIPSM  
DRREI FF RDIERGDIVIGRISSIREFGFFMVLCILGSGIMRDIAHLEITALCPLRDVPSHSN  
HGDPL SYYQTGDIIRAGIKIDDRYHEKLAVSLYSSSLPHLSGIKLGVISS  
EELPLYRRSVELN SNSLESYENVMQSSLGFVNPGVVEFLLEKLGI  
DES NPPS LMRGLQSKNFSEDFASALRK KQSASWALKCVKIGVDYFKVGRHVDAMNEY  
NKALEIDKQNVEALVARGALYATKGSLNKA IEDFELALENCPTHRNARKYLC  
QTLVERGGQLEEEEKFLNAESYYKKALALDETFKDAED ALQKLHKYM  
MQKSLELREKQAEKEEKQKTKKIELTSAEKLRLKLLKEEKR  
LKKRKSTSSSS VSSADESVSSSSSSSSGHKRHKH  
KRNRSESSRSSRRHSSRASSNQIDQNRKDECYPVP ANTSASFLNH  
KQEVEKLLGKQDRLQYEKTQIKEKDRCP  
LSSSSLEIPDDFGVYSYLFKKL TIKQPQAGPSGDIPEEGIVIID  
DSSIHVTDPELDQVGQDMEVEDSGIDDPDHG

**Important features of the protein:**

**Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 138-155

**N-glycosylation sites:**

Amino acids 288-292; 508-512; 542-546

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 300-304; 472-476; 473-477; 517-521; 598-602

**N-myristoylation sites:**

Amino acids 218-224; 222-228; 271-277; 348-354

**Amidation site:**

Amino acids 52-56

**Cell attachment sequence:**

Amino acids 125-128

407/615

**FIGURE 403**

CCGAGGCGGAGGAGCCCCGAGGGGGCGCGAGCCCCCATGAATCATGTAGTCAATCATTTC  
CAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTCCGAACGTGCCAGCTCAGAATA  
GGAAAATAACTTGGGATTATATTGAAAGACATGGATCTTGCTGCCAACGAGATCAGCATT  
ATGACAAACTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAG  
AGAAGGCAATTGAAAAATTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCCC  
CGCAGTATCCTCTCCTTATAGTTGTGATAAGGTTCTCGCAACCTGGGATTAATCTTGCTCA  
CTGCCTACTTGTGATTCAACCTTCAGCCCATTAGCACCTGAGCCAGTGCTTCTGGAGCTC  
ACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTGCCATTGCCAAGAAGTACA  
TGTCAAGAAAATAAGGGAGTTCCCTCTGCATGGGGGTGATGAAGACAGACCCCTTCCAGACTTTG  
ACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCATTCTGCCAAGTGCAC TG  
GCTGTGCCAGAACACACTGAAGGTGATGCTCCTGGAAGACGCCAAGGAAATTGAGAGGC  
TCCATCCACTGGTGATCAAGACGGAAAGCCCTGTTGGAGGAAGAGATTCA GCATTTTG  
GCCAGTACCCCTGAGGCGACAGAAGGCTCTCTGAAGGGTTTCGCAAGTGGTGGCGCTGCT  
TTCTGAGCGGTGGTCCCATTCTTATCCATGGAGGAGACCTCTGAACAGATCACAAATGT  
TACGTGAGCTTTCTGTTCACTCACCTGCCATTCCAAAAGATGCCTCTTAAACAAAGT  
GCTCCTTCTTCACCCAGAACCTGTTGGGGAGTAAGATGCATAAGATGCCCTGACCTATT  
TCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTCCAGTGCCGAAGACATTGTC  
AGTCTGTGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCGACACCACCCACTGGAAGG  
TCTACGTTATAGCCAGAGGGTCCAGCCTTGGTCATCTGCGATGGAACCGCTTCTCAGAAC  
**TG**AGGAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGAAAACCAGGTTGAAAGGGAA  
AAATAAAACAAAACGATGAAACTGCAAAA

408/615

**FIGURE 404**

MDLAANEISIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIVVYK  
VLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHLMSLPIAKKYMSENKGVPLHG  
GDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKTGKP  
LLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFPPVFTHL  
PFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCQSVAMPIEPGD  
IGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

409/615

**FIGURE 405**

TGCCGGGCTCGGGGCGCCTGACTCTCCCTCACCTGCCTCCTGGGCTCCACTCGTCTGCCCTGGACTCCC  
GTCTCCTCCTGCTCCTCCGGCTTCCCAGAGCTCCCTCCTTATGGCAGCAGCTCCCGGTCTCCGGCGCAGCTTCT  
CAGCGGACGACCCCTCTCGCTCCGGGCTGAGCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGCGGG  
TTTGGCTGCTGCTTCCCCGCCGGTGCCACTGCCACCAGCCGCCCTGCTGCCGCCGCGGGATGCTCAG  
TAGCCCGCTGCCCGCCCCCGCATCCTGTGTCCTCGGAAGCCGTTGCTGCTGCAGAGTTGCACGAACATAGTC  
**ATGGTGTGCTGGGGAGTCCCAGCAGTGCAGCAGCTGGACACTTGGCAGGGCTTTGCTGGCTGCTGCTGCTG**  
CCCCTCATGCTACTCATCGTAGCCCGCCGGTAAGGCTCGTGTCTTCCCTACCTCTTAAGTGACTGCCAACAG  
CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTTCCCTGTCGACACCAACACCTGTAAA  
TTTGATGGGAATGTTAAGAATTGGAGACACTGTGACTTGCCTGTCAGTTCAAGTGCACAAATGACTATGTG  
CCTGTTGCTGCTCCAATGGGGAGAGCTACCAAGAATGAGTGTACCTGCGACAGGCTGCATGCAAACAGCAGAGT  
GAGATACTTGTGGTGTCAAGAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGC  
TCTGGAGAAACTAGTCAAAAGGAGACATCCACCTGTGATAATTGCCAGTTGGTGCAGAATGTGACGAAGATGCC  
GAGGATGTCGGTGTGTAATTGACTGTTCTCAACCAACTTCATGCCATCCCCTGCGCTTCTGATGGAAA  
TCTTATGATAATGCATGCCAAATCAAAGAAGCATGTCAGAAACAGGAGAAAATTGAAGTCATGTTGGGT  
CGATGTCAGATAACACAACACTACAAGTCTGAAGATGGGATTATGCAAGAACAGATTATGCAGAGAAT  
GCTAACAAATTAGAAGAAAGTGCAGAGAACACCCACATACTTGTCCGAACATTACATGGCTTCTGCATGCAT  
GGGAAGTGTGAGCATTCTATCAATATGCAGGAGCCATCTGCAGGTGTGATGCTGTTATACTGGACAACACTGT  
GAAAAAAAGGACTACAGTGTCTATACGTTCTCCGGTCTGTACGATTTCAGTATGTTAATCGCAGCTGTG  
ATTGGAACAATTGAGATTGCTGTCTGTGTTGGTGGCTCTGCATCACAGGAAATGCCAGAACAGAACAGA  
ATTCAACAGACAGAACAGAAAATACAGGGCACTACAGTTCAAGAACATACAACAGAGCGTCCACGGAGGTTAATCTAA  
AGGGAGCATGTTACAGTGGCTGGACTACCGAGAGCTGGACTACACAATACAGTATTATAGACAAAAGAATAA  
GACAAGAGATCTACACATGTTGCCTTGCAATTGTTGTAATTACACCAATGAAAACATGACTACAGCTATATT  
GATTATGTTGATGATATTGAAATAGTATACTTGTCTGATGTTCTGTAATGTAATAAAACTATTATA  
TCACACAAATATAGTTTCTTCCATGTTGTTATATAATAACTCAGTGATGAG

410/615

**FIGURE 406**

MVLWESPRQCSSWTLCEGFCWLPLLPMILLIVARPVKLAAPTSLSDCQPTGWNCSGY  
DDRENDLFLCDTNTCKFDGECLRIGDTVTCVCQFKCNNDYVPVCGSNGESYQNECYLRQ  
AACKQQSEILVVSEGSCATDAGSGSGDGVHEGSGETSQKETSTCDICQFGAECDEDAED  
VWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLGRQDNTTTTK  
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRCDAGY  
TGQHCEKKDYSVLYVVPGPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRO  
KQNTGHYSSDNTTRASTRLI

411/615

**FIGURE 407**

CTCGCAGCCAGCGCGCCGGGAAGGGCTCCTCCAGCGCCGAGCACTGGGCCCTGGCAG  
ACGCCCAAGATTGTGAGGAGTCAGCCAGTGGTGAGCGCTGTAATCTGAACCAGCTGT  
GTCCAGACTGAGGCCCATTTGATTGTTAACATACTTAGAAAATGAAGTGTCAATTAA  
CATTCCCTCTCCAATTGGTTAATGCTGAATTACTGAAGAGGGCTAAGCAAACCAAGGTGCTT  
GCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCGGCGCTCTCCCCTGTCCTCCACGACT  
CGCTCGGCCCTCTGGAATAAAACACCCCGAGCCCCGAGGGCCCAGAGGAGGCCGACGTGCC  
CGAGCTCCTCCGGGGTCCCGCCGAGCTTCTCTCGCCTCGCATCTCCTCGCG  
TCTTGGAC**ATG**CCAGGAATAAAAGGAACTCACTGTTACCATTCTGGCTCTGTCTTCAA  
GCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTGACCTGGATGCCAGTCAGGACAGT  
GTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCGAGGAGACATGATGTGTTA  
ACCAAAATGGCGGGTATTATGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATT  
ACCCCTACTCGACCCCCACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCAA  
ACTATCCCACGATCTCAGGCCTTATATGCCGTTGGATACCAAGATGGATGAAAGCAACC  
AATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAAGTGCACACCCACCAAGATGCA  
TCAATACTGAAGGGGGTACACCTGCTCTGCACCGACGGATATTGGCTCTGGAAGGCCAGT  
GCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCTGGAT  
CCTATTCTGTACATGCAACCCCTGGTTTACCTCAATGAGGATGGAAGGTCTGCCAAGATG  
TGAACGAGTGTGCCACCGAGAACCCCTGCGTGCACACCTGCGTCAACACCTACGGCTCTCA  
TCTGCCGCTGTGACCCAGGATATGAACCTGAGGAAGATGGCCTTGCAGTGATATGGACG  
AGTGCAGCTTCTCTGAGTTCCCTGCCAACATGAGTGTGAAACCAGCCGGCACATACTCT  
GCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAACGCTGCCAAGACATCAACGAAT  
GTGAGCACAGGAACACACGTGCAACCTGCGAGACAGTGTCTACAATTACAAGGGGCTTCA  
AATGCATCGACCCCATCCGCTGTGAGGAGCCTATCTGAGGATCAGTGATAACCGCTGTATGT  
GTCCTGCTGAGAACCCCTGGCTGAGAGACCAGCCCTTACCATTTGTAACCGGACATGGACG  
TGGTGTCAAGGACGCTCCGTTCCGCTGACATCTCCAAATGCAAGGCCACGACCCGCTACCTG  
GGCCTATTACATTCCAGATCAAACCTGGGAATGAGGGCAGAGAATTTCACATGCCGCAA  
CGGGCCCCATCAGGCCACCTGGTGTGACACGCCCATCAAAGGGCCCAGGAAATCCAGC  
TGGACTTGGAAATGATCACTGTCAACACTGTCTACAATTCAAGGGCAGCTCCGTATCCGAC  
TGCAGTATATGTGTCGAGTACCCATT**CTG**ACCTGGCTGGAGCCTCCGACGCTGCCCT  
CATTGGCACCAAGGGACAGGAGAAGAGAGGAAATAACAGAGAGAATGAGAGCGACACAGACGT  
TAGGCATTCTGCTGAACTTCCCGAAGAGTCAGCCCCACTTCTGACTCTCACCTGTA  
CTATTGCAACCTGTCACCCCTGCAGGACTTGCACCCCTGAGCTTCTATGACACAGTTATCAA  
AAAGTATTATCATGCTCCCTGATAGAAGATTGTTGGTGAATTTCAGGCTTCAAGGCTTCAAG  
TCCACTATTCAAAGAAAATAGATTAGGTTGGGGCTGAGTCTATGTTCAAAGACTGT  
GAACAGCTGCTGTCACCTCTCACCTCCACTCCTCTCACTGTTACTGCTTGC  
AAGACCCGGAGCTGGGGGAACCTGGAGTAGCTAGTTGCTTTGCGTACACAGAGAA  
GGCTATGTAACAAACACAGCAGGATCGAAGGGTTTAAAGAGAATGTTCAAACCATGC  
CTGGTATTTCACCCATAAAAGAAGTTCAAGTGTCTTAAATTGATATAACGGTTAAATTCT  
GTCTGTTCAATTGAGTATTAAAGGAAATGTCGTTAGAATTCCCTGAAAGGCCTTCAGA  
CACATGCTATGTTCTGCTTCCAAACCCAGTCTCCTCTCCATTAGCCCAGTGTCTTCTT  
GAGGACCCCTTAATCTGCTTCTTAAAGATTACCAATTGGATGGAATGCAGAGGTCT  
CCAAACTGATTAAATATTGAAGAGA

412/615

**FIGURE 408**

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQN  
GGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNCV  
DVDECATDSHQCNPTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYS  
CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSЛИRCDPGYELEEDGVHCSDMDECS  
FSEFLCQHECVNQPGTYFCSCPAGYILLDDNRSCQDINECEHRNHTCNLQQTСYNLQGGFKCI  
DPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVSGRSVPADIFQMQATTRYPGAY  
YIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRI  
YVSQYPF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 283-287, 296-300

**N-myristoylation sites.**

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,  
267-273, 310-316

**Aspartic acid and asparagine hydroxylation sites.**

amino acids 144-156, 181-193, 262-274

**Cell attachment sequence.**

amino acids 54-57

**Calcium-binding EGF-like.**

amino acids 131-166, 172-205, 211-245, 251-286

413/615

**FIGURE 409**

CCACCGCGTCCGGACGCGTGGTCGACTAGTTAGATCGCGAGCGGCCGCCGGCTCA  
GGGAGGAGCACCGACTCGCGCCGACCCCTGAGAGA**ATG**GTTGGTGCCATGTGAAGGTGATTGTT  
TCGCTGGTCTGTTGATGCCTGGCCCCGTGATGGGCTGTTCGCTCCCTATACAGAAGTGT  
TCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCACCCCTTACATGAAGCTGGG  
AAGATCCAAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCAGGACTGAACATGAAGAGT  
TATGCCGGCTCCTCACCGTAATAAGACTTACAACAGCACCTCTCTGGTTCTTCCA  
GCTCAGATAACGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGGGAGGTTCA  
TCCATGTTGGACTCTTGTGAAACATGGGCCTATGTTGTCACAAGTAACATGACCTTGCCT  
GACAGAGACTCCCGGACCACAACGCTCTCCATGCTTACATTGACAATCCAGTGGCACA  
GGCTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGTAGCACGGGAT  
TTATAACAGTGCATAATTCAAGTTTCCAGATATTCTGAATATAAAAATAATGACTTTAT  
GTCACTGGGAGTCTATGCAGGGAAATATGTCAGGCCATTGCACACCTCATCCATTCCCTC  
AACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGATGGATATTCTGAT  
CCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCTTGGATGAGAAG  
CAAAAAAAAGTACTTCCAGAACAGCAGTGCATGAATGCATAGAACACATCAGGAAGCAGAACTGG  
TTTGAGGCCTTGAAAACTGGATAAAACTACTAGATGGCAGCTTAACAAGTGATCCTTCTAC  
TTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGTGCACGGAACCTGAGGAT  
CAGCTTACTATGTGAAATTGTCACTCCAGAGGTGAGACAAGCCATCCACGTGGGAAT  
CAGACTTTAATGATGAACTATAGTTGAAAAGTACTTGCAGAGAAGATACTACAGTCAGTT  
AAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGATCTACAATGGCCAACGGAC  
ATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGGACTGGAAAGGATCCCAG  
GAATACAAGAACGGAGAAAAAAAGTTGGAAGATCTTAAATCTGACAGTGAAGTGGCTGGT  
TACATCCGGCAAGCGGGTGACTCCATCAGGTAATTATTGAGGTGGAGGACATATTTACCC  
TATGACCAGCCTCTGAGAGCTTGCATGATTATCGATTCTGAAAGGATGGGAT  
CCTTATGTTGG**TAA**ACTACCTTCCAAAAGAGAACATCAGAGGTTTCAATTGCTGAAAAGAA  
AATCGTAAAAACAGAAAATGTCATAGGAATAAAAATTATCTTTCATATCTGCAAGATT  
TTTCATCAATAAAATTATCCTTGAAACAAGTGAGCTTTGTTTTGGGGGGAGATGTTACT  
ACAAAATTAAACATGAGTACATGAGTAAGAATTACATTATTAACTTAAAGGATGAAAGGTATG  
GATGATGTGACACTGAGACAAGATGTAAAATTAGGGTCTGAATAGGAAGTT  
ATTCTTCTAAGAGTAAGTGAAAAGTGCAGTTGTAACAAACAAAGCTGTAACATCTTTCTG  
CCAATAACAGAACAGTTGGCATGCCGTGAAGGTGTTGAAATATTATGGATAAGAATAGCTC  
AATTATCCCAAATAATGGATGAAGCTATAATAGTTGGGGAAAAGATTCTCAAATGTATAA  
AGTCTTAGAACAAAAGAATTCTTGAATAAAAATTATATAAAAAGTAAAAAAAAAA

414/615

**FIGURE 410**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGRELSLV  
GPFPGLNMKSYAGFLTVNKTYSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGP  
YVVTSNMTLDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQFFQI  
FPEYKNNDFYVTGESYAGKYVPAIAHLIHSINPRevKINLNGLAIGDGYSDESIIGGYAEF  
LYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFFEILDKLLDGDLTSDPsyFQNVTCGSNYY  
NFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNTFNDGTIVEKYLREDTVQSVKPWLTEIMNNY  
KVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKWKIFKSDSEVAGYIRQAGDFHQV  
IIRGGGHILPYDQPLRAFDMINRFIYKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

415/615

FIGURE 411

GCAAGCCAAGGCGCTGTTGAGAAGGTGAAGAAGTCCGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT  
CTACATGCCGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGCTACCGCACCTACCGCTGTGCCAACCC  
CCTGGCCACACTCTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGTCACGGCCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGCACCTCATGACCAATACGACCCGCTACTCCAA  
GCGCTTCGCCGTCTTCCTGTCGAGGTGAGTGAGAACAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT  
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTCATGCTCAGTGGC  
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCC  
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGTGGCTTACCCACAGCGGCCAAGATTGAAGCGCTGCGCT  
GGCCTTCCTGCGCAGAACCTGCGGGCGTGCACATCAAGTTACCGACATCAAGGAGATCCCGCTGTGGATCTA  
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGAGAACAAACCGCTACATCGTCATCGA  
CGGGCTGCGGGAGCTAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAACGAAGCTGCCACAGGTGGTAC  
AGATGTGGCGTGCACCTGCAGAACGACTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCCTAACAGCCTCAA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCCACTCCATCTCAGCCT  
CCACAACCTGCGAGGAGATTGACCTCAAGGACAACAAACCTCAAGAACCATCGAGGGAGATCATCAGCTTCCAGC  
GCACCGCCTCACCTGCCCTAACGCTGGTACACCACATGCCCTACATCCCCATCCAGATCGGCAACCTCACCAA  
CCTGGAGGCCCTCACCTGAACCGCAACAAAGATCGAGAACGAGATCCCCACCCAGCTTCTACTGCCGAAAGCTGCG  
CTACCTGGACCTCAGCCACAACCTGACCTCCCTGCCGACATCGGCCCTCTGCGAGAACCTCCAGAACCT  
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCGGGAGCTCTCCAGTGCAGGAGCTGACGAGATCGAGTGC  
GGGCAACAAACGCTGCTGAGTCAGTGCCTCCAGGGTGGGGAGCTGACCAACCTGACGAGATCGAGTGC  
CAACCGGCTGGAGTGCCTGCCTGCGAGCTGGCAGTGCCACTGCTCAAGCGCAGCGGCTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG  
GCCGGCCCAGCACAGCAAGCAGCAGCAGGCCCTCGCGCTGGCAGGAGCCTGGGGCAGGCCCTAGCTTCTCCAG  
AACTCCCGGACAGCCAGGACAGCCCTCGCGCTGGCAGGAGCCTGGGGCCTGTGAGTCAGGCCAGAGCGAGA  
GGACAGTATCTGTTGGGCTGGCCCTTTCTCCCTCTGAGACTCACGTCACGCCCCAGGGCAAGTGTGTTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTGATAATCAGGGCTCTCCCTGGAGGCCAGCTCTGCCCAAGGGCTGAG  
CTGCCACCGAGGCTCTGGGACCCCTCACTTCTGTTGTTGTTCTCCATCTCCACCTCTTCATCC  
AGATAACTTATACATTCCAAGAAAGTTCAAGGCCAGATGGAAGGTGTTCAAGGAAAGGTGGCTGCCTTCCCC  
TTGTCCTTATTAGCGATGCCGCCGGCATTTAACACCCACCTGGACTTCAAGGAGTGGTCCGGGGCAGACAG  
CCATGGGACGGTCACCCAGCTGCCGGCTGGCTCTGGGCTCGGGTCCAGGGCAGGCCCTCCAGCTGGA  
AAGGCCAGGCTGGAGCTGCCTTCTCAGTTTGTGGCAGTTTGTGTTTTTTTTAACTCAA  
AAACAATTTTTAAAAAGCTTGAAAATGGATGGTTGGTATTAAAAAGAAAAAAACTTAAAAAA  
AAAAGACACTAACGGCCAGTGAGTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGCCAGAC  
TGAACGTGTTCTCCCTGGGAGGGTGTCTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT  
CTATTTGTTCTGGGAGGGAGTTTTGTTGTTGTTGTTGGTTTTGGTGTCTTGTGTTCTTCTCCTCC  
ATGTGTTCTGGCAGGCACTCATTCTGTTGCTGTCGGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
ACTCGGGTTGGCTAATCCCGGATGAAACGGTGTCCATTGCCACCTCCCTCTCGTGCCTGCCCTGCCCTCTCCA  
CGCACAGTGTAAAGGAGCCAAGAGGGAGCCACTTCGCCAGACTTGTGTTCCACCTCTGCGGAGGGTGT  
CCAGTGCCACCGCTGCCCTCCGCTGCTCCATCAGCCCTGCGCCACCTGGTCTCATGAAGAGCAGACACTTA  
GAGGCTGGTGGGAATGGGGAGGTGCGCCCTGGGAGGGCAGGGCGTTGGTCCAAGGCCGGTCCCTGGCG  
CTGGAGTGCAACAGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTAGATCACTCGGGTCCCCACCTT  
AGAAGGGTCCCGCCTAGATCAATCAGTGGAGACTAAGGCACGTTTAGAGTCTCTGTCTTAATGATTATGT  
CCATCCGTCTGTCGTCATTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAAACCATGAAGCAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAA  
ATCTATAACAGAAAAAA

416/615

**FIGURE 412**

MRQTIIKVIKFILICITYVYYVHNIKFVDCTVDIESLTGYRTYRCAHPLATLFKILASFYIS  
LVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKRF  
AVFLSEVSENKLRLQLNLNNEWTLDKLQRQLTKNAQDKLELHLFMLSIGIPDTVFDLVELEVKL  
ELIPDVTIIPPSIAQLTGLKEIWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWIYSLK  
TLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSINNEGT  
KLIVLNSLKKMANLTELELIRCDLERIPHHSIFSLHNQEIIDLKDNNLKTIEEIIISFQHLHRLT  
CLKLWYNHIAYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLTFLPADIG  
LLQNLQNLAITANRIETLPPELFQCRKLRALHGNVLQSLPSRVGELETNLTQIELRGNRLEC  
LPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

417/615

**FIGURE 413**

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGTTTGAGCTCATC  
 TTCATCATCATATGAGGAATAAGTGGTAAACCTTCAAACATACA**ATGAGACTCATCAGAA**  
 ACATTACATATTTGTAGTATTGTTATGACAGCAGAGGGTGTGCTCCAGAGCTGCCAGAAG  
 AAAGGAAACTGATGACCAACTGCTCAAACATGTCCTAAGAAAGGTTCCGCAGACTTGACCC  
 CAGCCACAAACGACATGGATTATCCTATAACCTCCTTCAACTCCAGAGTCAGATTTC  
 ATTCTGTCTCCAAACTGAGAGTTGATTCTATGCCATAACAGAACTCAACAGCTGGATCTCA  
 AAACCTTGAATTCAACAAGGAGTTAAGATATTAGATTGCTTAATAACAGACTGAAGAGTG  
 TAACTTGGTATTACTGGCAGGTCTCAGGTATTAGATCTTCTTTAATGACTTGCACCCA  
 TGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTGAGTGGGCAA  
 AAATACAAAATCAGATTCCAGAAAATTGCTCATCTGCATCTAAATACTGCTTCTTAGGAT  
 TCAGAACTCTCCTCATTATGAAAGAAGTAGCCTGCCATCTAAACACAACAAAATGCACA  
 TTGTTTACCAATGGACACAAATTCTGGGTTCTTTGCCGTATGGAATCAAGACTTCAAAAAA  
 TATTAGAAATGACAAATATAGATGGCAAAGCCTAAGTTGTAAGTTATGAAATGCAACGAAATC  
 TTAGTTAGAAAATGCTAACAGACATGGTTCTATTGCTTAATAAAGTGTATTACTCTGGGACG  
 ACCTTTCTTATCTTACAATTGTTGGCATACATCAGTGGAACACTTCAGATCCGAAATG  
 TGACTTTGGTGGTAAGGCTTATCTTGACCACAATTCAATTGACTACTCAAATACTGTAATG  
 GAACTATAAAATTGGGACATGTACATTCAAGGTGTTACATTCAACAGGATAAAATCTATT  
 TGCTTTGACCAAAATGGACATAGAAACCTGACAATATCAAATGCAACAAATGCCACACATGC  
 TTTCGGAAATTATCCTACGAAATTCAAATATTAAATTGCCAATAATATCTAACAGACG  
 AGTTGTTAAAAGAACTATCCAACGTGCTCACTTGAAAATCTCATTTGAATGGCAATAAAC  
 TGGAGACACTTCTTAGTAAAGTGTCTTGCTAACACACACCCTGGAACACTTGGATCTGA  
 GTCAAAATCTTACAAACATAAAATGATGAAATTGCTCATGCCAGAAACTGTGGTCAATA  
 TGAATCTGTACATAAAATGTCATTGCTTCTCAGGTTGCTTGGCCAAAAGTATTCAA  
 TACTTGACCTAAATAACCAAACTCAAACGTACCTAAAGAGACTATTCACTGATGGCCT  
 TACGAGAACTAAATATTGCAATTAAATTCTAACTGATCTCCCTGGATGCGATCATTCTAGTA  
 GACITTCAGTTCTGAACATTGAAACTTCATTCTCAGGCCATCTCTGGATTGTTGTCAGA  
 GCTGCCAGGAAGTTAAAATGCGGGAAAGAAATCCATTCCGGTGTACCTGTGAATTAA  
 AAAATTCTCATTCAAGCTTGAACATATTCAAGGGTCACTGATGGTTGGATGGTCAGATTAC  
 CCTGTGAATACCCCTTAAACCTAAGGGAAACTAGGTTAAAAGACGTCATCTCCACGAATTAT  
 CTGCAACACAGCTCTGTGATTGTCACATTGTTGTTATTGCTAGTCTGGGGTTGGCTG  
 TGGCCTTCTGCTGTCCTCAATTGATCTGCCCTGGTATCTCAGGATGCTAGGTCAATGACAC  
 AACATGGCACAGGGTTAGGAAACACACCAAGAACAACTCAAGAGAAAATGTCGATTCCACG  
 CATTATTCTACACAGTGAACATGATTCTCTGGGTTGAAAGATGAATTGATCCCCAATCTAG  
 AGAAGGAAGATGGTTCTATCTGATTGCTTTATGAAAGCTACTTGACCCCTGGCAAAGCA  
 TTAGTGAAAATATTGTAAGCTCATTGAGAAAAGCTATAAGTCATCTTGTGTTGTCTCCC  
 ACTTGTCCAGAATGAGTGGGCCATTATGAAATTCTACTTTGCCACCACAATCTTCCATG  
 AAAATTCTGATCATATAATTCTTACTGGAACCCATCCATTCTATTGCAATTCCACCA  
 GGATCATAAAACTGAAAGCTCCTCTGGAAAAAAAGCATACTGGAAATGGCCCAAGGATAGGC  
 GTAAATGTGGCTTTCTGGGAAACCTTCGAGCTGCTATAATGTAATGTTATTAGCCACCA  
 GAGAAATGTATGAACATGCAACGACATTCAAGAGTTAAATGAAGAGTCTCGAGGTTCTACAAATCT  
 CTCTGATGAGAACAGATTGCTAT**AAAATCCCACAGTCCTGGGAAGTTGGGACACATACA**  
 CTGTTGGGATGTACATTGATACAACCTTATGATGGCAATTGACAATATTATTAAAATAAA  
 AAATGGTTATTCCCTCATATCAGTTCTAGAAGGATTCTAAGAATGTATCTTATAGAAACA  
 CCTTCACAAGTTATAAGGGCTTATGAAAAAAAGGTGTTCATCCCAGGATTGTTATAATCATG  
 AAAATGTGGCCAGGTGCAGTGGCTCACTCTGTAATCCCAGCACTATGGGAGGCAAGGTGG  
 GTGACCCACAGGGTCAAGAGATGGAGACCATCTGGCCAAACATGGTAAACCCCTGTCTACT  
 AAAATACAAAATAGCTGGGCGTGTGGTGCAGGCCCTGTAGTCCCAGCTACTTGGGAGGCT  
 GAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGCAGTTGCGATGAGCTGAGATCGAGGCCACTG  
 CACTCCAGCCTGGTGACAGAGCGAGACTCCATCTCAAAAAAAAGAAAAAAAGAAAAAA  
 ATGGAAAACATCCTCATGCCACAAAATAAGGTCTAATTCAATAATTATGATACATTATGT  
 AATATAATATTACATGCCACTAAAAGAATAAGGTAGCTGTATATTCTGGTATGGAAAAAA  
 CATATTAAATATGTTATAAAACTATTAGGTTGGTGCACAAACTAATTGTTGTTTGCCTATTGAA  
 TGGCATTGAAATAAAAGTGTAAAGAAATCTATACAGATGTAGTAACAGTGGTTGGGCTGG  
 GAGGTGGATTACAGGGAGCATTGATTCTATGTTGTGTTCTATAATGTTGAATTGTT  
 TAGAATGAATCTGTATTCTTATAAGTAGAAAAAAATAAGATAGTTTACAGCCT

418/615

**FIGURE 414**

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCNSMSLRKVPADLTPATTLDLSYNLLFQL  
QSSDFHSVSKLRVLILCHNRIQQLDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSF  
NDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLPILN  
TTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNI DGKSQFVSYEMQRNLSLENAKTSVLLLNKV  
DILWDDLFLLQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFYIQ  
QDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLN FANNILTDELFKRTIQLPHLKTLI  
LNGNKLETLSLVSCFANNTPLEHLDLSQNLLQHKNDENCSPETVVNMNLSSYNKLSDSVFRCL  
PKSIQILDNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRSLSVLNIEMNFILSPS  
LDFVQSCQEVKTLNAGRNPFRCTCELKNIQLETYSEVMMVGWSDSYTCEYPLNLRGTRLKDV  
HLHELSCNTALLITIVVIMVLGLAVAFCCFLHFDLPWYLRMLGQCTQTWHVRVRKTQEQQLKR  
NVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI  
FVLSPNFVQNEWCHYEFYFAHHNLFHENSDHIILILLEPIPFYCIPTRYHKLKALLEKKAYLE  
WPKDERRKGGLFWANLRAAINVNVLATREMYELQFTTELNEESRGSTISLMRTDCL

419 / 615

**FIGURE 415**

CGGACGCGTGGCGGACCGGTGGCCTGGCAAGGGCGGGCGCCGGCGAGCCACCTCTCCCCCTCCCCGC  
 TTCCCTGTCGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCGGCCCTGGGGCTGACAGT  
 CGGCAAAGTTGGCCCGAAGAGGAAGTGGCTCAAAACCCCGGCAGGTGGCGACCAGGCCAGACCAGGGCGCTCG  
 CTGCCTGCGGGCGGGCTGTAGGCAGGGCGCCCGACTGGCGAGACCCGGGGCTTCAGGAGCCGGCCGGAG  
 AGAAGAGTGGCGGGCGGAGCGAGAACAACTCCAAAGTGGCAAAGGACCCGGCTACTCCCCGGGCTGCCG  
 CGGCCTCCCCGGCCCGAGGCTGGCATCCAGAGTACGGCTGAGGCGGGCATGGAGCCCCCTGGGGAGGCCG  
 CACCAGGGAGCCTGGCGCCGGCTCGCCGAGCCCCTGGTAGACCACAGAAAGCTCCGGACCCCTTCCAG  
 GCACCTCTGGACAGCCAGGATGCTGTGGCACCCCTCCTCCTCCTGGAGGCGCTGGCCATCCAG  
 ACCGGATTATTTTCAAATCATGCTTGTGAGGACCCCCAGCAGTGTCTTAGAAGTGCAGGGCACCTAACAGA  
 GGGCCCTGGTCCGGGACAGCGCACCTCCCTGCCAAGTGCACCTGGCTCATCCTGGGAGCAAGGAACAGACTG  
 TCACCATCAGGTTCCAGAAGCTACACCTGGCTGTGGCTCAGAGCGCTTAACCCCTACGCTCCCTCTCCAGGCC  
 TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCGGGGCACGTCACCATCACTTACAGCTATG  
 CTGGGGCCAGAGCACCCATGGGCCAGGGCTCTGCTCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG  
 AGTTTCAGTGCCTGAACCACCGCTGTGTATCTGCTGTCAGCGCTGTGATGGGGTGTGATGCCTGTGGCGATGGCT  
 CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCTGGCTGACCCCAAGACCCGTCCTCCCTGCCTTGCATG  
 TCACCTGGAGGACTCTATGGGTCTTCTCCTCTGGATACACACCTAGCCTCAGTCTCCACCCCTGGAGTGGCT  
 CCTGCCATTGGCTGCTGGACCCCATGATGGCCGGCTGGCGCTGGCTCACAGCCCTGGACTTGGGCT  
 GAGATGCAGTGCATGTGTATGACGGCCCTGGGGGGCTGAGGCTCCGACTACTGGTAGTCTCACCCACTTCA  
 GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCAGGCTGTTGTCCTACACAGATTGCTTGGAGCA  
 ATGGTCGTGGCTCAATGCCACCTACCATGTGGGGCTATTGCTTGGCTGGAGACAGCCCTGGCTTGGACT  
 CTGGCCTGGAGCTGGCGAAGGCCTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT  
 GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGGCACCT  
 CTGGTGCCACAGCCTGCTACCTGCCCTGCAACTACCAGACTTCTGCTGATGGAGCAGATGAGA  
 GACGCTGTCGGCATTGCCAGCCTGGCAATTCCGATGCCGGACGAGAAGTGCCTGTATGAGACGTGGGTGTGCG  
 ATGGGCAGCCAGACTGTGCGGACGGCAGTGAGTGGGACTGCTCTATGTCCTGGCCCAAGGTCTATACAG  
 CTGCAGTCATTGGCAGCTAGTGTGCGGCTGCTGGCTACGCCCTGGCTGCAAGCTCTATGCC  
 TTCGCACCCAGGAGTACAGCATCTTGGGGGGCTCCGGATGGAGGCTGAGATGTGCAAGCAGCAGGACCCCC  
 CTTCTACGGGCAGCTCATGGGGGGCTGCCATCCACCTGTAAGAAGACTTCTACAGAGAATCTAATGATA  
 ACTCAGTGTGGCAACCTGCGTTCTGCTACAGATCTACGCCAGGATATGACTCCAGGGGTGGCCCAAGGTG  
 CCCGCCGTGCTAGCGGGCCGCTTGATGCGACGCCCTGGTACGCCGTCTCCGCCCTGGGCTTGTCCCTCGAA  
 CCAACACCCGGCTGGGGCTCTGGAGGAGATCCCAGGTACACACTTCTGCTGCTTGGGGCTAGATG  
 GTGGCACAGGTCCAGCCCGTGGGGGGCAGTGGTAGGCGAAGATGGGAGCAGGGCACCCCCACTGCCCATCA  
 AGGCTCCCCCTCCCATCTGCTAGCACCGTCTCAGGCCCCACTACTGTCCCTGAAGCCCCAGGGCACTGCCCTCAC  
 TGCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAAGGCCCTGCGAGGCCCTGTTGCCCCAGCCTGGGGCCCC  
 CAGGACCAACCGGAGCCCCCTGGACCCACACAGCACTTGGGCCCTGGAAGATGAGGAGGATGTGACTGG  
 TGCCACTGGCTGAGCCGGGGGTGTGGTAGCTGAGGAGGATGAGGCCACTGCTACCTTGAAGGGGACCTGGGG  
 CTCTACTGAGGCCTCTCCCTGGGGCTCTACTCATAGTGGCACAACCTTTAGAGGTGGGTGAGCCTCTGCTATAAAAGT  
 ACCACTTCCCTCCCTGTCCTGGATTTCAAGGGACTTGGTGGGCTCCCGTTGACCCCTATGAGCTGCTATAAAAGT  
 TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTAACGTGGCCATGGCCAGACACCCAGTC  
 TCACCAACCTGCTCCCCACGCCACCATGGGTGGCTGTTTAAAAGTAAAGTCTAGAGGATCATA  
 GGTCTGGACACTCCATCTTGCCAAACCTCTACCCAAAAGTGGGCTTAAGCACCAGAATGCCAATTAACTAGAGA  
 CCCTCCAGCCCCAAGGGAGGATTGGGAGAACCTGAGGTTTGCCATCCACAACTCCCTACAGGGCTGG  
 CTACACAAAAAGAGTGCACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTAAAAATAAA  
 GGAATCATACTC

420/615

**FIGURE 416**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLGGALAHPDRIIFPNHACEDPPAVILLEVQGTLQRPLVRDSRTSPANCTWLILG
SKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPQLPGGNVTITYSYAGARAPMG
QGFLLSYSQDWLMC1QEEFQCLNHRCVSAVQRCGVDACGDGSDEAGCSSDPFPGLTPRPVPS
LPCNVTLEDFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRLAVRTALDLGFGDAHVYDG
PGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLPWRDPC
GLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEECPGCPPGHFPCGAAGTSGATAACYLPA
DRCNYQTFCADGADERRCRHCQPGNFRCRDEKCVYETWVCDGQPDCAAGSDEWDCSYVLPRKV
ITAAVIGSLVCGLLLIVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSYQQLIAQGA
IPPVVEDFTENPNDNSVLAGNLRSLLQILRQDMTPGGGPGARRRQRGRLMRRLVRRRLRWGLLP
RTNTPARASEARSQVTPSAAPLEALDGTTGPAREGGAVGGQDGEOAPPLPIKAPLPSASTSPA
PTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLPSLGPPGPTRSPPGPHTAVLADEDVVLL
VPLAEPGVWVAEAEDEPLL
```

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

421/615

**FIGURE 417**

GTCGTTCCCTTGCTCTCGGCCAGTCCTCCCTGGTCTCCTCAGCCGCTGCGGAGGAGAGCACCGGA  
 GACGCGGGCTGCAGTCGGCGGCTTCTCCCGCTGGCGGCCAGCAGTCACATGGGTGTTGGAGGTAGATGGCTCCCG  
 AGCCTCCCTGCCGCTCCCTCCTGCCCGGCCAGCAGTCACATGGGTGTTGGAGGTAGATGGCTCCCG  
 GCCCAGGAGCGGGCTGGATGCCGCTGGCAGAAGCAGCCGATTCCAGCTGCCCGCGGCCGGCG  
 CCCCTGCAGTCCCCGGTCAGCCATGGGACCTCTCGAGCAGCAGCACCGCCCTGCCCTGCAGCCGCATC  
 GCCCGCCGAGCCACAGCCACAGATGATCGGGCTCCCTCCTGCTGGATTCCCTAGCACACCACAGCTCAG  
 CCAGAACAGAAGGCTCGAATCTCATGGCACATACCAGCATGGACCTGACCAACACAGCCTGCCGCTCTG  
 GACAAGTGTCCAGCAGGAACCTATGCTCTGAGCATTGTAACCAACAGCCTGCCGCTCTGAGCAGTTGCCCT  
 GTGGGGACCTTACCGCATGAGAATGGCATAGAACATGCCATGACTAGTCAGGACATGCCATGGCAATG  
 ATTGAGAAATACCTTGCTGCTGCTGACTGACCGAGAACATGCACTGGCCACCTGGCATGTTCCAGTCAACGCT  
 ACCTGTGCCCCCCTACGGTGTGCTGTGGGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCG  
 TGTAAGCAGTGTGCTGGGTACCTCTCAGATGTGCTCTAGTGTGATGAAATGCAAAGCATACACAGACTG  
 CTGAGTCAGAACCTGGTGGTGTCAAGCCGGGACCAAGGAGACAGACAACGTGTGGCACACTCCGCTCC  
 TCCAGCTCACCTCACCTCCCTGGCACAGCCATCTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCC  
 TCCTCCACTTATGTTCCAAAGGCATGAACCTAACAGAACATCTCTGCCCTGTTAGACCAAGGACT  
 AGTAGCATCCAGGAAGGGACAGTCCTGACAACACAAGCTCAGCAAGGGGAAGGAAGACGTGAACAAGACCC  
 CCAAACCTTCAGGTAGTCACCACAGCAAGGCCACACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG  
 GCCACTGGGGCGAGAAGTCCAGCACGCCATCAAGGCCCAAGAGGGACATCCTAGACAGAACCTACACAAG  
 CATTTGACATCAATGACATTGGCCCTGGATGATTGCTGTTTCTGCTGCTGGTGTGTTGAGTGTGGT  
 TGCACTTCGGAAAAGCTCGAGGACTCTGAAAAAGGGGCCCGCAGGATCCCAGTGCCTGGAAAGGCA  
 GGGCTGAAGAAATCCATGACTCCAACCGAGAACCGGGAGAAATGGGATCTACTACTGCAAGCTGCTGCC  
 ATCTGAAGCTTGTAGCAGCCAAGTGGAAAGGAGATATCTATCAGTTCTTGCATGCCAGTGTG  
 AGGGAGGTTGCTGCTTCTCCAATGGTACACAGCCGACACAGCAGGGCTACGCACTCTGCAGCACTGGACC  
 ATCCGGGGCCCCGAGGCCAGCCTGCCAGCTAACTAGCCTGCCAGCAGGGAGAAACGATGTTGGAG  
 AAGATTCTGGGCTGATGGAAGACACCACCCAGCTGGAAACTGACAACACTAGCTCTCCGATGAGCCCC  
 CTTAGCCGAGCCCCATCCCCAGCCCCAACGCAAACCTGAGAATTCCGCTCTCTGACGGTGGAGCCT  
 CAGGACAAGAACAGGCTCTCGGGATGAGTCGGAGCCCTCTCCGCTGTGACTCTACATCCAGCGCTCC  
 TCCCGCTGAGCAGGAACGGTTCTTATTACCAAAGAAAAGAACAGCACAGTGTGCGGCAGGTACGCC  
 CCCTGTGACTTGCAGCCATCTTGATGACATGCTCCACTTCTAAATCTGAGGAGCTGCC  
 ATTCCCGAGCTGAGGACAAACTAGCCTGGCTATTGAAATATTGGAGTCAGGACAGGCCAGGAAGCC  
 CAGACCCTCTGGACTCTGTTATAGCCATCTCCTGACCTGCTGTAAGAACATAAGGGACT  
 ATTTAGTGGCAGGGTGGTTTTAAATTCTGTTCTGTTCTGTTCTGTTGTTGGGTGTTGTTGTTG  
 GTGTGTGTGTGTGTGTGTGTGTGTTAACAGAGAAATATGGCAGTGCTTGAGTTCTTCTC  
 TCTCTCTCTTTTTAAATAACTCTCTGGAAAGTTGTTATAAGCCTTGCAGGTGTA  
 ACTGTTGTGAAATACCCACCAACTAAAGTTTTAAGTCCATATTCTCCATT  
 TTGCCITCTTATGTATTTCAGATTCTGAGGCTCTTCAAGGATT  
 TGCACCTTAAATTACTAACCTACATAATGCACTGACTTTCCCACACACTGGATTGAGGCTCTAAC  
 TTCTTAAAGTATAATGGCATCTGTAATCCTATAAGCAGTCCTTATGCTCTAACATT  
 CAACACTTCTTT  
 AAAAACAAATATTACTATTTTATTGTTGTCCTTATAAAATTCTTAAAGGATTAAGAAAATTAAAGA  
 CCCATTGAGTTACTGTAATGCAATTCAACTTGA  
 GTTATCTTAAATATGCTTGTGTTAGTCATATT  
 CTGAAACCTGACCAACTATTGCTGATTGTTCTACCTGGACACCGTGTAGAATGCTGATTACTGTAC  
 TCTCTTATGCTAATGCTCTGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTGCTATT  
 TAAGTGGCTT  
 GACAACGTGGCCACCAAGAACACTGACCTTACCTTCTGTTAGGATTGAGCTGTTCTGGAAACACATT  
 GGAAAGTCAAATCAAGTGCCTGGCGCCCTTCCATAGAGAAATTGCGCAGCTTGTCTTAAAGATGTCTT  
 TTTTTATACACATACTCAATAGGTCCTGCTCAAGGCCCTGGCTGTGGGATT  
 CCTCACCATT  
 ACTTTAATTAAAAATGGCTGCACTGTAAGAACCTTGTCTGATATATTGCA  
 ACTATGCTCCATTACAAATG  
 TACCTTCTAATGCTCAGTTGCCAGGTCCAATGCAAAGGTGGCGTGGACT  
 CCCTTGTGTGGGGTTGTGG  
 GTAGTGGTGAAGGACCGATATCAGAAAAATGCCCTCAAGTGTACTA  
 ATTAAACATTAGGTGTTGTT  
 AAAAAAAA

422/615

**FIGURE 418**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pi: 8.22, NX(S/T): 8
MGTPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTAQPEQKASNLIGTYRHVDRATGQ
VLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFRHENGIKEKCHDCSQPCPWPMIEKLPCAAL
TDRECTCPPGMFQSNTCAPHTVCVGWGVKKGTETEDVRCKQCARGTFSDVPSVMKCKAY
TDCLSQNLVVIKPGTKETDNVCGLPSFSSTSPPGTAIFFPRPEHMETHEVPSSTYVPKGMM
STESNASSASVRPKVLSSIQEGETVPDNTSSARGKEDVNKTLPNLQVNVHQQGPHHRHILKLLPS
MEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRKSSRTLK
KGPRQDPSAIVEKAGLKKSMPTQNREKWIIYCNGHGIDILKLVAACQVGSQWKDIYQFLCNAS
EREVAAFSNGYTADHERAYAALQHWTIRGPEASIAQLISALRQHRRNDVVEKIRGLMEDTTQL
ETDKLALPMSPSPLSPSPNAKLENSALLTVERPSPODKNKGFVDESEPLLRCDSSTSSGS
SALSRNGSFITKEKKDTVLRQVRLPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLE
IIGVKSQEASQTLLSDVYSHLPDLL
```

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 350-370

423/615

**FIGURE 419**

ATGGCTGGTACGGCGGGCCGGCAGGGGACCGGGGCCGGCGCCGGGAGCAGCTGCAGGGAGCCCTGA  
ATCACCGCCTGGCCGACTCCACCATGAACGTGCGCTGCAGGAGCTGGAGCTGGCAGCAACGTGGGATTCCAG  
AAGGGGACAAGACAGCTTAGGCTCACGCACGCAGCTGGAGCTGGCTTAGCAGGTGCCTCTACTGCCTGGCT  
GCACTGCTCTGGCTGCCTGTGGCCCTAGGGTCCAGTACACAGAGACCCATCCCACAGCACCTGCCTTACA  
GAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGTGAGGCCCTGTGAGGACTTTAC  
CAGTTCTCCTGTGGGGCTGGATTGGAGAACCCCTGCCCAGTGGCGTTCTCGCTGGAACACCTCAACAGC  
CTCTGGGACAAAACCAGGCCACTGAAGCAGCTGAAACACCACTTCACACTCCAGCACTGAAGCTGAG  
CAGAAGACACAGCCTCTACCTATCTGCCTACAGGTGGAGCGCATTGAGGAGCTGGAGGCCACTGAGA  
GACCTCATTGAGAAGATGGGGTGGAAACATTGGGGCCCTGGGAGGACACACTTATGGAGGTTGAAG  
GCAGTAGCAGGGACCTACAGGGGCCACCCATTCTCACCGTACATCAGTGCCTACTAAGAGTTCAAACAGC  
AATGTTATCCAGTGGACAGTCTGGCTCTTCTGCCCTCGGGATTAACAGAACTGCAAATGAG  
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACCTGGGATGCTGCTGGGTGGCGGCCACCTCCACGAGG  
GAGCAGATGCAGCAGGTGCTGGAGATACTGGGAAACATCACAGTGCCTGGAGGCCACAGTGCCTGGGAGG  
GAGGAGAAGATCTACCACAAGATGACCATTCGGAGCTGCAAGGCTCTGGGCCCTCATGGACTGGCTTGAGTTC  
CTGTCTTCTGCTGTCAACCATTGGAGTTGAGTGACTCTGAGCTGTGGTGTATGGGATGGATTATTCAG  
CAGGTGTAGAGCTCATCACCGCACGGAAACAGCATCTGAACAATTACCTGATCTGGAACCTGGTGC  
ACAACCTCAAGCCTGGACCGACGCTTGAGTCAGCACAAGAGAAAGCTGCTGGAGACCCCTATGGCA  
TCTGTGTGCCAGGGTGCAGACCTGCATCTCCAACACGGATGACGCCCTGGCTTTGGGTCACTCTTC  
GTGAAGGCCACGTTGACCGGCAAAGCAAAGAAATTGCAAGAGGGGATGATCAGCGAAATCGGACCGCATTGAG  
GAGGCCCTGGGACAGCTGGTTGGATGGATGAGAAGACCCGCCAGGCCAGGAGAAAGCAGATGCCATCTAT  
GATATGATTGGTTCCAGACTTATCTGGAGGCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTCT  
GAAGATTCTTCTTCCAAAACATGTGAATTGACAACCTCTGCAAGGTTATGGCTGACAGCTCCGA  
CCTCCCAGCCAGACAGTGGAGCATGACCCCCAGACAGTGAATGCCACTACCTTCAACTAAGAATGAGATC  
GTCTCCCCGCTGGCATCTGCAGGCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACCTCGGTGC  
GGTGTGGTCACTGGGCATGAGTTGACGCATGCCATTGATGACCAAGGGCGCAGTATGACAAAGAAGGG  
CGGCCCTGGTGGCAGAATGAGTCCTGGCAGCCTCCGGAACACAGGCCCTGCATGGAGGAACAGTACA  
TACCAAGGTCAATGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGAGAACATTACTGACAACGGGG  
GCTGCCTACAATGCTTACAAGCATGGCTGAGAAAGCATGGGAGGAGCAGCAACTGCCAGCCGTGGGCTCACC  
AACCACCAAGCTCTCTCGTGGGATTGCCCAGGTGCTGGCTCGGCACACAGAGAGCTCTCACGAGGG  
CTGGTGACCGACCCCCACAGCCCTGCCGCTTCCGCCTGCTGGGACTCTCTCCAACCTCCGTGACTCTCG  
CACTTCGGCTGCCCTGCGCTCCCCATGAACCCAGGGCAGCTGAGGTGTTGAGGATCAGGG  
GAAATGGCCAGCTGTCACCAGACCTGGGCAGCTCTCTGACAAAGCTGTTGCTTGGGTTGGAGGAAGCAA  
ATGCAAGCTGGCTGGGTCTAGTCCTCCCCCAGGTGACATGAGTACAGACCCCTCTCAATCACCACATTG  
TGCCCTGCTTGGGGTGCCTCCAGCAGAGCCCCACCATCACTGTGACATCTTCCGTGTCACCCT  
GCCTGGAAGAGGTCTGGTGGGAGGCCAGTCCCATAGGAAGGAGTCTG

424/615

**FIGURE 420**

MNVALQELGAGSNVGFOKGTRQLLGSRTQLELVLAGASLLAALLLGCLVALGVQYHRDPSHS  
TCLTEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNP LPDGRSRWNTFNSLWDQNQAIL  
KHLLENTTFNSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNI TGPPWDQDNFME  
VLKAVAGTYRATPFFT VYISADSKSSNSNVIQVDQSGFLPLSRDYYLNRTANEKVLTAYLDYM  
EELGMILLGGRPTSTREQM QQVLEIQLANITVPQDQRRDEEKIYHKMSISELQALAPSMDWL  
EFLSFLLSPL ESDSEPVVVYGM DYLQQVSELINRTEPSILNNYLIWNLVQKTTSSLDRRFES  
AQEKLLETLYG TKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMISEIRTA F  
EEALGQLVWMDEKTRQA AKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLY  
NFSAKVMADQLRKPPS RDQWSMT PQT VNAYYLPTKNEIVFPAGILQAPFYARNHPKALNFGGI  
GVVMGHELTHAFDDQGREYDKEGNL RPWWQNESLAAFRNHTACMEEQYNQYQVN GNERLNGRQT  
LGENITDNGGLKAAYNAYKAWLRKHGEEQOLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGL  
VTDPHSPARFRVLGTLNSRDFLRHF GCPVGSPMNPGQLCEVW

**Type II Transmembrane domain:**  
amino acids 32-57

425/615

## FIGURE 421

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGCTGCAGGCCCTGCCCATGCGCCGCC  
GCCTCTCCGCACGATGTTCCCTCGCGGAGGAAAGCGGCCAGCTGCCCTGGGAGGACGGCAG  
GTCCGGGTTGCTCTCGGCCCTCCCTCGGAAGTGTTCGTCTCCACCTGTTGTCGGCTG  
CCTCTCGCTGGGTTCTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGACGTGGCCCG  
GGCAGTCAGGGACAAGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCTCAGAGCCGCC  
CCCTGAGCACTGGAAAGAAGACGCATCCTGGGCCCCACCGCCTGGCAGTGCTGGTGCCTT  
CCGCGAACGCTCGAGGAGCTCTGGTCTTCGTGCCACATGCGCCGCTTCCTGAGCAGGAA  
GAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACCTCAGGTTCAACCAGGCAGC  
GCTCATCAACGTTGGCTCCTGGAGAGCAGCACAGCACGGACTACATTGCCATGCACGACGT  
TGACCTGCTCCCTCTAACGAGGAGCTGGACTATGGCTTCCTGAGGCTGGCCCTTCACGT  
GGCCTCCCCGGAGCTCCACCCCTCTACCACTACAAGACCTATGTCGGCGGCATCCTGCTGCT  
CTCCAAGCAGCAGTACCGGCTGTGCAATGGATGTCCAACCGCTCTGGGCTGGGCCGCGA  
GGACGACGAGGTTCTACCGGCGCATTAAGGGAGCTGGCTCCAGCTTCCGCCCTCGGGAAT  
ACAACGGTACAAGACATTGCGCACCTGCATGACCCAGCCTGGCGGAAGAGGGACCAAGAA  
GCGCATCGCAGCTAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGGAGGCCTGAACACTGT  
GAAGTACCATGTGGCTCCCGCACTGCCCTGTCTGTGGCGGGCCCTGCACTGTCTCAA  
CATCATGTTGGACTGTGACAAGACGCCACACCCCTGGTCACATTCAAGCTGAGCAGTGGATGGAC  
AGTGAGGAAGCCGTACCTACAGGCCATATTGCTCAGGCTCAGGACAAGGCCCTAGGTCGTGG  
GCCAGCTCTGACAGGATGTGGAGTGGCAGGACCAAGACAGCAAGCTACGCCATTGCGAGCCA  
CCCGGCCGCCAAGGCAGGCTGGCTGGGCCAGGACACGTGGGTGCCTGGGACGCTGCTGC  
CATGCACAGTGATCAGAGAGAGGCTGGGTGTGTCCTGTCGGGACCCCCCTGCCTTCCTGC  
TCACCCCTACTCTGACCTCCTCACGTGCCAGGCCCTGTGGTAGTGGGAGGGCTGAACAGGA  
CAACCTCTCATCACCCCTACTCTGACCTCCTCACGTGCCAGGCCCTGTGGTAGTGGGAGGG  
CTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAA

426/615

**FIGURE 422**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531  
><subunit 1 of 1, 327 aa, 1 stop  
><MW: 37406, pi: 9.30, NX(S/T): 1  
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHIVACLSLGFFSLLWLQLSCSGDVARAVRG  
QGQETSGPPRACPPEPPPEHWEEDASWGPHEVLAFLVPFRERFEELLVFPHMRRFLSRKKIRH  
HIYVLNQVDHFRFNRRAALINVGFLESSNSTDYIAMHDVDLPLNEELDYGFPEAGPFHVASPE  
LHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDDEFYRRIKGAGLQLFRPSGITTGY  
KTFRHLHDPAWRKRDQKRIAAQKQEKFVDRREGGLNTVKYHVVASRTALSVGGAPCTVLNIMLD  
CDKTATPWCTFS

**Signal peptide:**  
amino acids 1-42

**Transmembrane domain:**  
amino acids 29-49 (type II)

**N-glycosylation site.**  
amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 27-31

**Tyrosine kinase phosphorylation site.**  
amino acids 226-233

**N-myristoylation site.**  
amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

427/615

**FIGURE 423**

CCATCCCTGAGATCTTTATAAAAAACCCAGTCTTGCTGACCAGACAAAGCATACCAGATC  
TCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGCTGGATGCT  
GCTTCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAAC TGCCCTC  
TCCACGGATCAGCTGCCAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTGTTTT  
GTCACCAAAATCTGGATGGATGCAGATCTGGCTGCCAGAAGCGGCCCTCTGGAAAAC TGGT  
GTCTGTGCTCAGTGGGCTGAGGGATCCTCGTGTCCCTGGTGAGGAGCATTAGTAACAG  
CTACTCATACATCTGGATTGGCCTCCATGACCCACACAGGGCTCTGAGCCTGATGGAGATGG  
ATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAATCCCTCCACCAT  
CTTAAACCCCTGGCCACTGTGGGAGCCTGTCAAGAACAGCACAGGATTCTGAAGTGGAAAGATTA  
TAACTGTGATGCAAAGTTACCCATGTCTGCAAGTTCAAGGACTTAGGGCAGGTGGGAAGTCAG  
CAGCCTCAGCTTGGCGTGCAGCTCATGGACATGAGACCAGTGTGAAGACTCACCTGGAA  
GAGAATATTCTCCCCAAACTGCCCTACCTGACTACCTTGTCAATGATCCTCTTTCTT  
TTTCTCACCTTCATTCAGGCTTCTGTCTGCTTCCATGTCTGAGATCTCAGAGAATAATA  
ATAAAAATGTTACTTTATAAAAAAAAAAAAAAA

428/615

**FIGURE 424**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965  
<subunit 1 of 1, 175 aa, 1 stop  
<MW: 19330, pI: 7.25, NX(S/T): 1  
MLPPMALPSVSWMILSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM  
ADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISSNSYSYIWIGLHDPTQGSEPDGDGWEWSSTD  
VMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

**Important features:**

**Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

429/615

**FIGURE 425**

CGGACGCGTGGGCCGCCACCTCCGGAAACAAGCCATGGTGGCGGCACGGTGGCAGCGCGTGG  
CTGCTCCTGTGGCTGCGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTCAAGGCGGTC  
AACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCTGGTGGTGAAT  
GTGGCCAGCGAGTGGGCTTACAGACAGCAGCACTACCGAGCCCTGCAGCAGCTGCAGCAGAC  
CTGGGCCCCCCACCACCTTAACGTGCTGCCTTCCCCTGCAACCAGTTGGCCAACAGGAGCCT  
GACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGACCTACAGTGTCTCATCCCCATGTT  
AGCAAGATTGCAGTCACCGTACTGGTGCCATCCTGCCTCAAGTACCTGGCCCAGACTTCT  
GGGAAGGAGCCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGGTGGTAGGG  
GCTTGGGACCCAACTGTGTCAGTGGAGGAGGTCAAGACCCAGATCACAGCGCTCGTGAGGAAG  
CTCATCCTACTGAAGCGAGAAGACTTATAACCCACCGCGTCTCCTCCACCACCTCATCCCG  
CCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAGAGACCCACTGA  
CTCTCCTCCTTACTCTTATGCCATTGGTCCCATCATTCTGTGGGGAAAAATTCTAGTAT  
TTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCTGGCCAATGAGAGCTTGTGACCAG  
TGAATCACCAGCCGATACGAACGTCTGCCAACAAAATGTGTGGCAAATAGAAGTATATCAA  
GCAATAATCTCCCACCAAGGCTCTGTAAACTGGGACCAATGATTACCTCATAGGGCTGTTG  
TGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCACCCAAATAGGAGGCATTC  
AATGAACATTTTGATATAACCAAAAAATACTTGTATCAATAAAACTTGCATCCAAC  
ATGAATTCCAGCCGATGATAATCCAGGCCAAAGGTTAGTTGTGTTATTCCTCTGTATTA  
TTTCTTCAATTACAAAAGAAATGCAAGTTCAATTGTAACAATCCAACAAATACCTCACGATATA  
AAATAAAATGAAAGTATCCTCCTCAAAAA

430/615

**FIGURE 426**

MVAATVAAAWLLLWAAACAAQEQDFYDFKAVNIRGKLVSLKYRGSVSLVVNVASECGFTDQH  
YRALQQLQRDLGPHHFNVLAFCNCQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTGAH  
PAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEVRPQITALVRKLILLKREDL

431/615

**FIGURE 427**

CAGTTCTGAAATCAATGGAGTTAATTAGGGAATACAAACCAGCC**ATG**GGGGTGGAGATTGCC  
TTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTCTT  
CTCCAGCCAGTTCCAACTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGCTT  
GCCGGCCACTCAT**TG**AAGTGTTTGAGTAAAGTATTTAGAATACTGTTGACTTCTTCAT  
GATTTAATAACCATCCTTGCAGTAAAGTTATGAGGCTTAGGGGAATGTCAACCCTCAAATT  
TTGTTATACTAGATGGCTTCATTACCCACCACTATTTAAGGTCCCTTATTTAGGTT  
AAGGTTCAATTGACTTGAGAAAGTGCCTCTGCAGCTTATTGATTTGTTATCTTCACTA  
TTAATTGTAACGATTAAGAATAAGAGCAGCAGACCTCTAGGAGAATATTTATCCCTG  
GGTGCCCCCTGACACATTATGTAGTGATCCCACAAATGTGATTGTTAATTAAATGTTATTCT  
AATATTAGTACATTCACTGAGTGTATGTAATATGAAATAACCAGAATCTATTCTAAAAGTTTG  
AGTATATTTCAACTAGATTTGTATAGAAAGACTGAATAGTGATG

432/615

**FIGURE 428**

MGVEIAFASVILTCLSLLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

433/615

**FIGURE 429**

CCAAAGT GATCAT TTGAAAAAGAGATATCCACATCTCAAGCCCATAAAAGGATAGAAGCTG  
CACAGGGCAGCTTACTTACTCCAGCACCTCCCTCTCCAGGCAATGGTGCTGACCATCTT  
GGGATACAATCTCATGGATACGAGGTTTAACATCATCAGCCCAAGCAACAATGGTGGCAAT  
GTT CAGGAGACAGTGACAATTGATAATGAAAAAAATACGCCATCGTTAACATCCATGCAGGA  
TCATGCTCTTCTACCACAATTTGACTATAAACATGGCTACATTGCATCCAGGGTGCTCTCC  
CGAAGAGCCTGCTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAATCTCAA  
TGGTACATCTATGAGAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTGGGTCAAG  
TACAAC CCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCTGCTTGGGTACCCATTGAG  
AAACTCTGCAAACATATCCCTTGATATAAGGGGAAGTGGTTGAAAACACACATAATGTCGGT  
GCTGGAGGCTGTGCAAAGGCTGGCTCTGGCATCTGGGAATTCAATCTGTGCAGACATT  
CATGTTTAGGATGATTAGCCCTCTGTTTATCTTCAAAGAAATACATCCTGGTTACAC  
TCAAAAGTCAAATTAAATTCTTCCCAATGCCCAACTAATTGAGATTCA GTCA GAAAATA  
TAAATGCTGTATTATA

434/615

**FIGURE 430**

&gt;&lt;ss.DNA57834

&gt;&lt;subunit 1 of 1, 176 aa, 1 stop

&gt;&lt;MW: 19616, pI: 7.11, NX(S/T): 0

MVLTIFGIQSHGYEVFNIISPSNNGGNQETVTIDNEKNTAIVNIHAGSCSSTTIFDYKH  
GYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWWVKYNPLESLIK  
DWDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV**Important features:****Signal peptide:**

Amino acids 1-26

**N-myristoylation sites:**

Amino acids 48-54;153-159;156-162;167-173

435/615

FIGURE 431

GC GTGGGG**ATGT**CTAGGAGCTCGAAGGTGGTGGCCTCTCGGTGCTGCTGACGGCGCCA  
CA GTGGCCGGCGTACATGTGAAGCAGCAGTGGACCAGCAGAGGCTCGTGACGGAGTTATCA  
GAGACATTGAGAGGCCAATTGGAAAAAGAAAACATTGCTTTGGGAGAACAGATTATT  
TGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAATCAT**G**  
**ACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTGTGTGTGTTGATGGAGA**  
GTAGCTTAGTGTATCTTCATCTTTGGTCAGTGCCTTAAACTGATCAAATAAA  
GGACAGTGGGTCAATAAGTTACTGCTTCAGGGTCCCTTATATCTGAATAAAGGAGTGTGGG  
CAGACACTTTGGAAGAGCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGGTCACTGTC  
CAGTGCTTAGGGTTGTTACTGAGAAGCAGTGCAGCAGCTTGTGAGAAGGAAGGGATGGATAGTA  
GCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGGAGAACATCGACCTCAG  
AAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

436/615

**FIGURE 432**

MSRSSKVVLGLSVLLTAATVAGVHVKKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILTE  
QLEAEREKMLLAKGSQKS

437/615

**FIGURE 433**

GAATTCTGTCTCGGCACTCACCCCCGGCCGGACAGGGAGCTTCGCTGGCGCGCTTGGCCGGCGACAGGA  
CAGGGTCTGGGACGCCATCTGCCATCGTCCGGAGAGAAATTACAGATCCGCAGCCCCGGGATGGGCGGCC  
CGCTGCCGCTGCTGCTGGCCTCTCCTCCCCGCGCTGGCGTAGAGCTATCACTGAGGAAGGGAAAGAACCA  
AGCCTTACCCGCTATTCCCGGACCTTCCAGGGAGCTGCAAACAGGACACACCACGGCTGTTATCCCTCCCTC  
ACGCCAGTGGTACCAAGCCCTACCGCCTCTGCCTCAAACACACAGTTGGACACATAACTT  
TCTGAACATAAAGGTGCAATTAACTGCTCAATGTAACCTAATATACCAAGGACACCAAACTTCTGG  
TGGAAAGATGGGAAGGAATTGCTTGGGGACATCATCGAATCAGCTTATCAGATGAGTTACAGCA  
ATAATCGCTCCTCAGCATACACAGTGCGAGCTGAGACAATGGCTGATATCTGAAGATGAAAATAAAC  
ATATGAAGAGATCGTCTGATCCCCTACATCGAAGTACAAGGACTCCTCACTTACTAAGCAGCCTGAGAGC  
ATGAATGTCACCAAGAACACAGCCTCACCTCACCTGTCAGGCTGTTGGCCGCGCTGAGCCCGTCAACATTTC  
TGGGTTCAAAACAGTAGCCGTGTTACGAACAGCCTGAAAAAATCCCCGGCGTCTAAGTGTCCAGGCGTACG  
GAGATGGCGGTCTTCAGTTGAGGGCCACAATGACAAAGGGCTGACCGTGTCCCAGGGAGTGCAGATCAACATC  
AAAGCAATTCCCTCCCCACCAACTGAAGTCAGCATCGTAACAGCACTGCACACAGCATTCTGATCTCTGGGTT  
CCTGGTTTGATGGATACTCCCCGTTAGGAATTGCAAGCATTGAGCTAAGGAAGCTGATCCGCTGGGTAATGGC  
TCAGTCATGATTTAAACACCTCTGCCTTACACATCTGTAACCAATCAAGCAGCTGCAAGCCCTGGCTAATTAC  
AGCATTGGGTTCTCGCATGAATGAAATAGGCTGGTCTGCACTGAGGCCCTGGATTCTAGCAAGCACGACTGAA  
GGAGCCCCATCAGTAGCACCTTAAATGTCAGTGTGTTCTGAATGTAATCTAGTGTAAATGTGGACATCAGATGG  
ATGAAGGCTCCGACTAAGCAGCAGGATGGAGAACTGGTGGGCTACCGGATATCCACGTGAGCTGAGGG  
ATTTCAGGAGCTTGGAGGAATTGGCCAAGATGGCAGCGAGCTGGATCTGTTCAAGTCCACAATGCT  
ACGTGCACAGTGGGATTGCAAGCCGTACCAAGAGGGGAGTTGGGCCCTCAGTGATCCAGTGAAAATATTATC  
CCTGCACACGGTTGGTAGATTATGCCCTCTCAACTCCGGCGCTGGCAACGCAGATCTGTGTCATCATC  
TTGGCTGCTTTGTGGATTATTTGATTGGGTTGATTATACATCTCCTGGCATCAGAAAAAGAGTCCAG  
GAGACAAAGTTGGGAATGCATTACAGAGGGATTCTGAATTAGTGGTGAATTATAGCAAAGAAATCCTTC  
TGTGGCGAGCCATTGAACCTACATAGCTGGGAGTCAGTGAGGAACACTAAAATAAGATGTT  
GTGATTGACAGGAATTCTCTAATTCTGGAAAATTCTGGGAGAGTTGGGCTGTAATGGAAGGAAAT  
CTTAAGCAGGAAGATGGACCTCTGAAAGTGGCAGTGAGACCATGAAAGTGGACAACCTTCACATCGGGAG  
ATCGAGGAGTTCTCAGTGAGCAGCTGAGGAGCTGGATCTGAGCTTCTGAGCTTCTAGGTG  
TGTATAGAAATGAGCTCTAAGGCATCCAAAGCCCATGGTAATTCTCCTCATGAAATACGGGACCTGCAT  
ACTTACTTACTTATTCCGATTGGAGACAGGACCAAGCATTCTCCTGAGACACTATTGAAGTTCTGAG  
GATATTGCCCTGGGAATGGAGTATCTGAGCAACAGGAATTCTCATCGAGATTAGCTGCTCGAAACTGCATG  
TTGCGAGATGACATGACTGCTGTTGCGGACTTCGGCTCTCTAAGAAGATTACAGTGGCATTATTACCGC  
CAAGGCCGATTGCTAAGATGCCCTTAAATGGATGCCATAGAAAGTCTGCAAGCCGAGTCTACACAAGTAA  
AGTGTGTGGGCAATTGGCGTACCATGTGGAAATACGTACGCCATCCATTCTGGGCTCAG  
AACCAGAGATGACTATCTCTCATGCCACAGGTGAAGCAGCCGAAGACTGCCATGAGCTGAACTGAT  
GAAATAATGTACTCTGCTGGAGAACCGATCCCTAGACCGCCACCTTCTAGTATTGAGGCTGCAGCTAGAA  
AAACTCTGAAAGTTGCCCTGAGCTGGAGACCGACGCTTACAGTCAAGACATACAGTTGCTGGAGAGC  
TCTGGGGCTGGCCAGGGCCCACCTTCTGCTTCAAGCAGAAGCTGAAACTGACCTGACTCTAATTGCCCTC  
TGCACCTCCCGCTGCCATCAGTGTTGAGCTGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG  
CTGAATGGGGCAGTGGAGAATGGGAAGATCTGACTCTGCCCTCTGCTGAGCTGAGCTGAGCTGAGCT  
GTTTACCGGGGAGAGACTTGTAGGAATGGGCTCTGGCTCCATTGAGCATGCTGCCCTGGGAAGCTCA  
TTGCCCGATGAACTTTGTTGCTGAGACTCTCAGAAGGCTCAGAAGTCTGAGCTGAGCTGAGCTGAG  
GACATTCCAAAATCAAGCCAATTCTCTGCTGAGGAATCCAATTGTACCTGATGTTGGTATTGTCTT  
CCTTACCAAGTGAACCTCATGCCCAAGCACCAGATGATGTTAAGGAAGCTGTCATTAAAAATACATAA  
TATATATTATTAAAGAGAAAAATATGTATATCATGAAAAGACAAGGATATTAAATAAAACATTACTTA  
TTTCACTTCACTTATCTGCATCTTAAATAAGCTCAGCTGCTCCCTGATATTAAACCTTGTACAGAGTTG  
AAGTTGTTTTCAACTCTTCTTCTTCACTTAAATTAAGTAAAGAATGATAATTCTGATATGGCTTCCATAA  
TGACTTGGCTCTGGCTTGTGATGTTGATAAGAATGATAATTCTGATATGGCTTCCATAAATAAAATTGAA  
ATAGGA

438/615

**FIGURE 434**

MGPAPLPLLGLFLPALWRRRAITEAREEEAKPYPLFPGPFPGLQTDHTPLLSLPHASGYQPALMFSPTOQGRPH  
 GNVAIPQVTSVESKPLPPLAFKHTVGHIIILSEHKGVKFNCISINVPNIYQDTTISWWKGKELLGGHHRITQFYPD  
 DEVTAAIASFSITSVQRSDNGSYICKMKINNEEJVSDPIYIEVQGLPHFTKQPESMNVTRNTAFNLTCQAVGPPE  
 PVNIFWVQNSSRVNEQPEKSPGVLTVPGLTEMAVFSCAEHNDKGLTVSQGVQINIKAIISPPTEVSRNSTAHSI  
 LISWVPGFDGYSPFRNCSTIQVKADPLGNGSVMIFNTSALPHLYQIKQLQALANYSIGVSCMNEIGWSAVSPWIL  
 ASTTEGAPSVAPlNVTVFLNESSDNVDIRWMKPPTKQQDGELEVGYRISHVWQSAGISKELLEVGQNGSRARISV  
 QVHNATCTVRIAATRGGVGPFSDPVKIFIPAHGWDYAPSSTPAPGNADPVLIFGCFCGFILIGLILYISLAI  
 RKRVQETKFGNAFTEEDSELVVNYIAKKSFCRRAIELTLHSLGVSEELQNKLVEDVVIDRNLLILGKILGEgefGS  
 VMEGNLKQEDGTSLKAVKTMKLDNSSHREIEEFLSEAAACMKDFSHPNVIRLLGVCIEMSSQGIPKPMVILPFMK  
 YGDLHTYLLYSRLETGPKHIPLQTLKFMVDIALGMEYLSNRNFHLRDLAARNCMRLDDMTVCVADFGLSKKIYS  
 GDYYRQGRIAKMPVKWIAIESLADRVTYTSKSDVWAFGVTMWEIRTRGMTYPYGVQNHEMYDYLLHGHRLKOPEDC  
 LDELYEIMYSCWRTDPLDRPTFSVRLQLEKLESLPDVVRNQADVIVYNTQLESSEGCLAQGPTLAFLDNIDPD  
 SIIASCTPRAAISVVTAEVHDSKPHGRYIINGGSEEWDLTSAPSAAVTAEKNSVLPGERLVRNGVSWHSSML  
 PLGSSLPDELLFADDSEGSEVLM

Signal sequence:	Amino acids 1-18
Transmembrane domain:	Amino acids 501-520
N-glycosylation sites:	Amino acids 114-118;170-174;207-211; 215-219;234-238;294-298;316-320;329-333; 336-340;354-358;389-393;395-399;442-446; 454-458;625-629
Tyrosine kinase phosphorylation sites:	Amino acids 675-683;865-873;923-930
N-myristoylation sites:	Amino acids 41-47;110-116;171-177; 269-275;275-281;440-446;507-513;535-541; 966-972
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 351-362
Tyrosine protein kinases specific active-site signature:	Amino acids 719-732

439/615

**FIGURE 435**

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTAGCACCACTGGATG  
TGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCACTGGCACACTGCTCCTCTTCGGCTTCCTG  
CCAAGC**ATG**GAATGCTGCCGTCGGCAACTCCTGGCACACTGCTCCTCTTCGGCTTCCTG  
CTCCTGAGTCCAGGACCGCACGCTCCGAGGAGGACGGACGGCTATGGATGCCTGGG  
CCATGGAGTGAATGCTCACGCACCTGCCGGGGAGGGCCTCTACTCTGAGGCGCTGCC  
AGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATAACAGAACATGCAGTAATGTGGACTGCCA  
CCAGAACGAGGTGATTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCACCATGGC  
CAGTTTATGAATGGCTTCCTGTGCTAATGACCCCTGACAACCCATGTTCACTCAAGTGCAA  
GCCAAAGGAACAACCCCTGGTGTGAACTAGCACCTAAGGTCTTAGATGGTACGCGTTGCTAT  
ACAGAATCTTGGATATGTGATCAGTGGTTATGCCAAATTGTTGGCTGCGATCACCAGCTG  
GGAAGCACCCTCAAGGAAGATAACTGTGGGCTGCAACGGAGATGGTCCACCTGCCGGCTG  
GTCCGAGGGCAGTATAAATCCCAGCTCCGCAACCAAATCGGATGATACTGTGGTTGCACTT  
CCCTATGGAAGTAGACATATCGCCTGTCTAAAAGGTCTGATCAGTCTATATCTGAAACC  
AAAACCCCTCCAGGGACTAAAGGTGAAAACAGTCTCAGCTCACAGGAACCTCCTGTGGAC  
AATTCTAGTGTGGACTTCCAGAAATTCCAGACAAAGAGATACTGAGAATGGCTGGACCACTC  
ACAGCAGATTTCATTGTCAAGATTGTAACCTGGGCTCCGCTGACAGTACAGTCCAGTTCATC  
TTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTCTTCCCTGCTCAGCAACCTGT  
GGAGGAGGTTATCAGCTGACATCGGCTGAGTGTACGATCTGAGGAGCAACCGTGTGGTTGCT  
GACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACCCAAAGCTTCAGGAGTGCAAC  
TTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGCCCTATGACCTCTACCATCCC  
CTTCCTCGGTGGAGGCCACCCCATGGACCGCGTGTCCCTCGTGTGGGGGGGATCCAG  
AGCCGGGAGTTCTGTGGAGGAGGACATCCAGGGCATGTCAGTCAGTGGAAAGAGTGG  
AAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTCAGTGCCTAA  
TGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTCAGATACCGTGTG  
GTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCCAAAACAAAGCCCCAC  
ATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAACCCAAAGAGAAACTCCAGTCGAG  
GCCAAGTTGCCATGGTCAAACAAGCTCAAGAGCTAGAAGAAGGAGCTGCTGTGTCAGAGGAG  
CCCTCG**TA**AGTTGTAAGACAGACTGTTCTATATTGAAACTGTTGTTAAAGAAAGCA  
GTGTCTCACTGGTTGTAGCTTCATGGTTCTGAAACTAAGTGTAAATCATCTCACCAAGCTT  
TTGGCTCTCAAATTAAAGATTGATTGATTTCAAAAAAAAAAAAAA

440/615

**FIGURE 436**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847
<subunit 1 of 1, 525 aa, 1 stop
<MW: 58416, pI: 6.62, NX(S/T): 1
MECCRRATPGTLLLFLAFLSSRTARSEEDRDGLWDAWPWSECRTCGGGASYSLRRCLSS
KSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVHHQFYEWLPVSNDPDNPCSLKCQAK
GTTLVVELAPKVLGDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVNGDGSTCRLVR
GQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDHLYLETKTLQGTKGENSLSSTGTFLVDNS
SVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCSATCGG
GYQLTSAECYDLRSNRVVADQYCHYY PENIKPKPKLQECNLDPASPASDGYKQIMPYDLYHPLP
RWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWL
AQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTAPHKEECIVPTPCYKPKEKLVEAK
LPWFQQAQELEEGA AVSEEPS
```

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

441/615

**FIGURE 437**

AACTGGAAGGAAAGAAAGAAGGTCA GCTTGGCC CAGATGTGGTTACCCCTGGTCTCCTGT  
CTTTATGTCTTTCTCCTCTTCTATTCTGTCA TCTCCCTACTTAAGTCTCAGGCCTGTCAGC  
AGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTCAGAGCAAACAGGACAACCTATGTTA  
TGGATGTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCCTGTGCTTCTGTGATC  
TCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTC **TGAA**ATCTGGCATGAGATG  
GCACAGGTGACCACGCAGAACGCCACCAGAAATCTGCCTGCCCTATTCCCTCCCAAGTCTGT  
TCTCTTATTGTCAACCTCAGCACAA CAGGCTGGGCCAATGGCATTACAGAGAAAGCAATCTG  
TGTGGCTAGTGGG CAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTGTAGCCACCT  
CCCTGTCA GCCAGTATTAACATGTCCCCCTCCCCCTGCCCGCGTAGATTCA GGACATT CGC  
CCCTGTGTGCCACCAA ACCAGGACTTCCCCTGGCTTGGCATCCCTGGCTCTCCTGGTAC  
CCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATTTCAAGCTCCGTTACTATGGCGATGGC  
CATGATGTTACAATCCC ACTTGCCTGAATAATCAAGTGGGAAGGGGAAGCAGAGGAAATGGG  
GCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCC TGAGGAAAAACCAAAGGGAAAGCAACAGG  
AACTTCTGCAACTGGTTTTATCGGAAGATCATCCTGCCTGCAGATGCTGTGAAGGGGCAC  
AAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAAGGTGTGTAAGGAAATAGAACAGTCTGCT  
GGGAGTCAGACCTGGAATTCTGATTCCAAACTCTTATTACTTTGGGAAGTCACTCAGCCTCC  
CCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACAA  
ATGTAGGTTACTAGTGAATAACCCAATGGTTCTCAATTATGCCCATGCCACCAAAACAATA  
AAACAAAATTCTCTAACACTGAAA